

Fig. 1

5'	9			18			27			36			45			54		
	GTG	GGC	ATG	GTG	GGC	AAC	GTC	CTG	CTG	GTG	CTG	GTG	ATC	GCG	CGG	GTG	CGC	CGG
	Val	Gly	Met	Val	Gly	Asn	Val	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg
	63			72			81			90			99			108		
	CTG	CAC	AAC	GTG	ACG	AAC	TTC	CTC	ATC	GGC	AAC	CTG	GCC	TTG	TCC	GAC	GTG	CTC
	Leu	His	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu
	117			126			135			144			153			162		
	ATG	TGC	ACC	GCC	TGC	GTG	CCG	CTC	ACG	CTG	GCC	TAT	GCC	TTC	GAG	CCA	CGC	GGC
	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly
	171			180			189			198			207			216		
	TGG	GTG	TTC	GGC	GGC	CTG	TGC	CAC	CTG	GTC	TTC	TTC	CTG	CAG	CCG	GTC	ACC	
	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	225			234			243			252			261			270		
	GTC	TAT	GTG	TCG	GTG	TTC	ACG	CTC	ACC	ACC	ATC	GCA	GTG	GAC	CGG	TAC	GTC	GTG
	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val
	279			288			297											
	CTG	GTG	CAC	CCG	CTG	AGG	CGG	CGC	ATC	3'								
	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile									

Fig. 2

5' GGC CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr

GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC TGC GTG ACC CAG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln

AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val

GTG GTC GTG GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr

Fig. 3

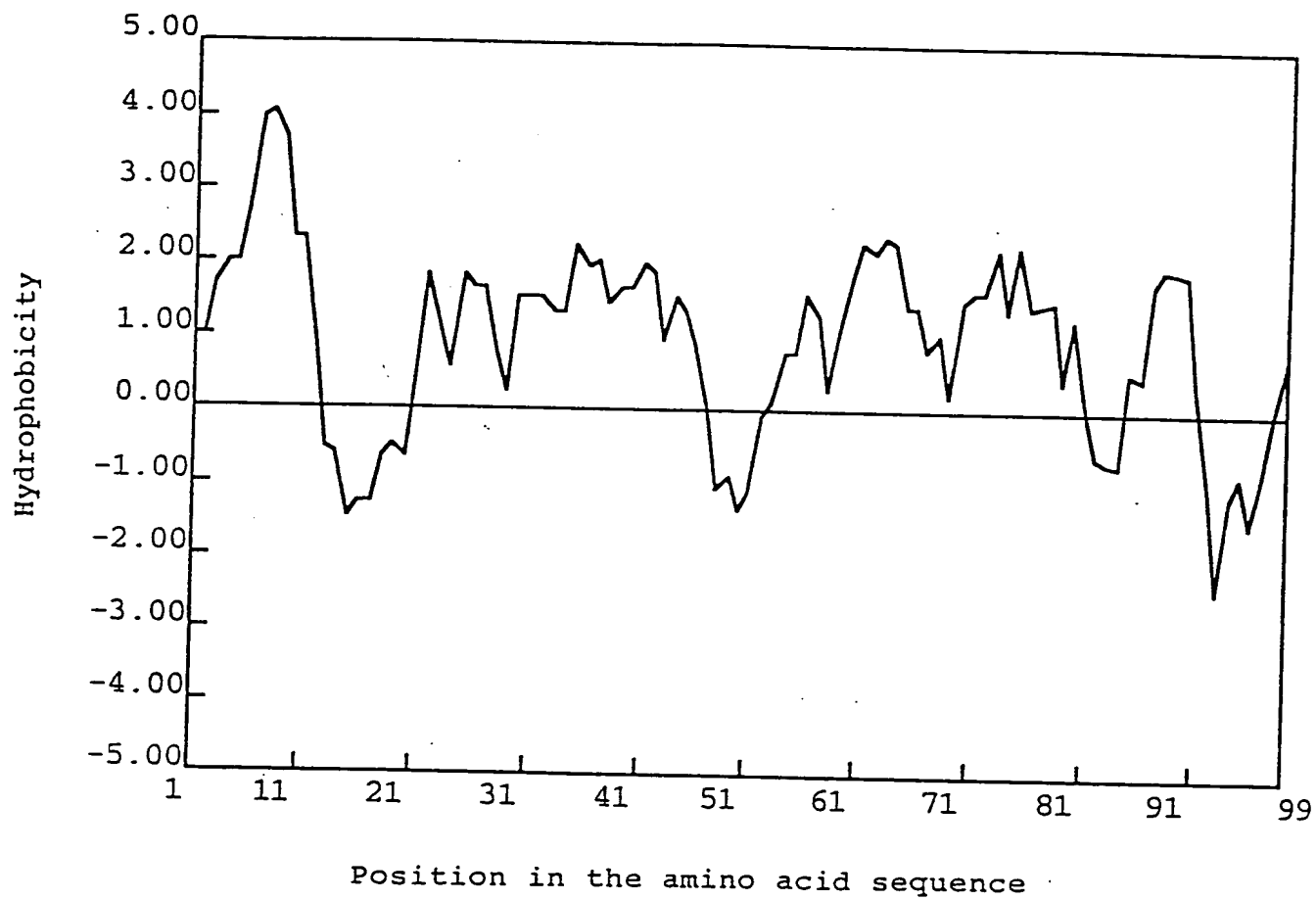


Fig. 4

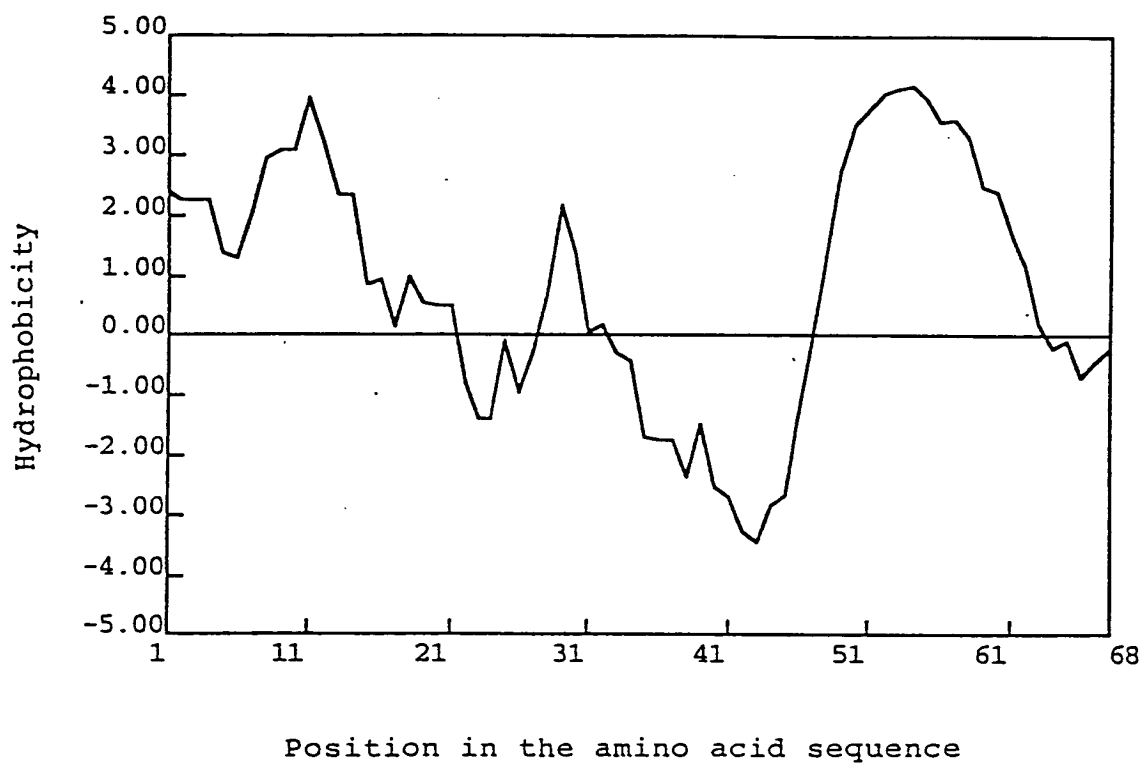


Fig. 5

p19P2	10	20	30	40	50
S12863	1 VGMVGNMLLV	LVFARVRLH	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF
	1 LGVSGNMLAI	IIILKQKEMR	NVTNHLIVNL	SFSDLLAVAM	CLPFTFVYIL
p19P2	60	70	80	90	100
S12863	51 EPRGWWFGG	LCHLVFLOP	VIIVVSVFTL	TTIAVDRYVW	LVHPLRRRI-
	51 MDH-WVFGET	MCKLNPEVQC	VSITVSIFSL	VLIAVERHQL	IINPRGWRN
p19P2	110	120	130	140	150
S12863	101 -----	-----	-----	-----	-----
	101 NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK
p19P2	160	170	180	190	200
S12863	151 -----GLLV	TVLLPLLVIL	LS-----	VRVSVKLRNR	VVPGCVTQSQ
	151 FPSDSHRLSY	TTLLLVLOYF	GPLCFIFICY	FKIYIRLKRR	NNMMDKIRDS
p19P2	210	220	230	240	250
S12863	201 ADWDRARRR	TFCLLVVVV	VFAICWLPFY
	201 KYRSSETKRI	NVMLLSIWA	-FAVCWLPLT

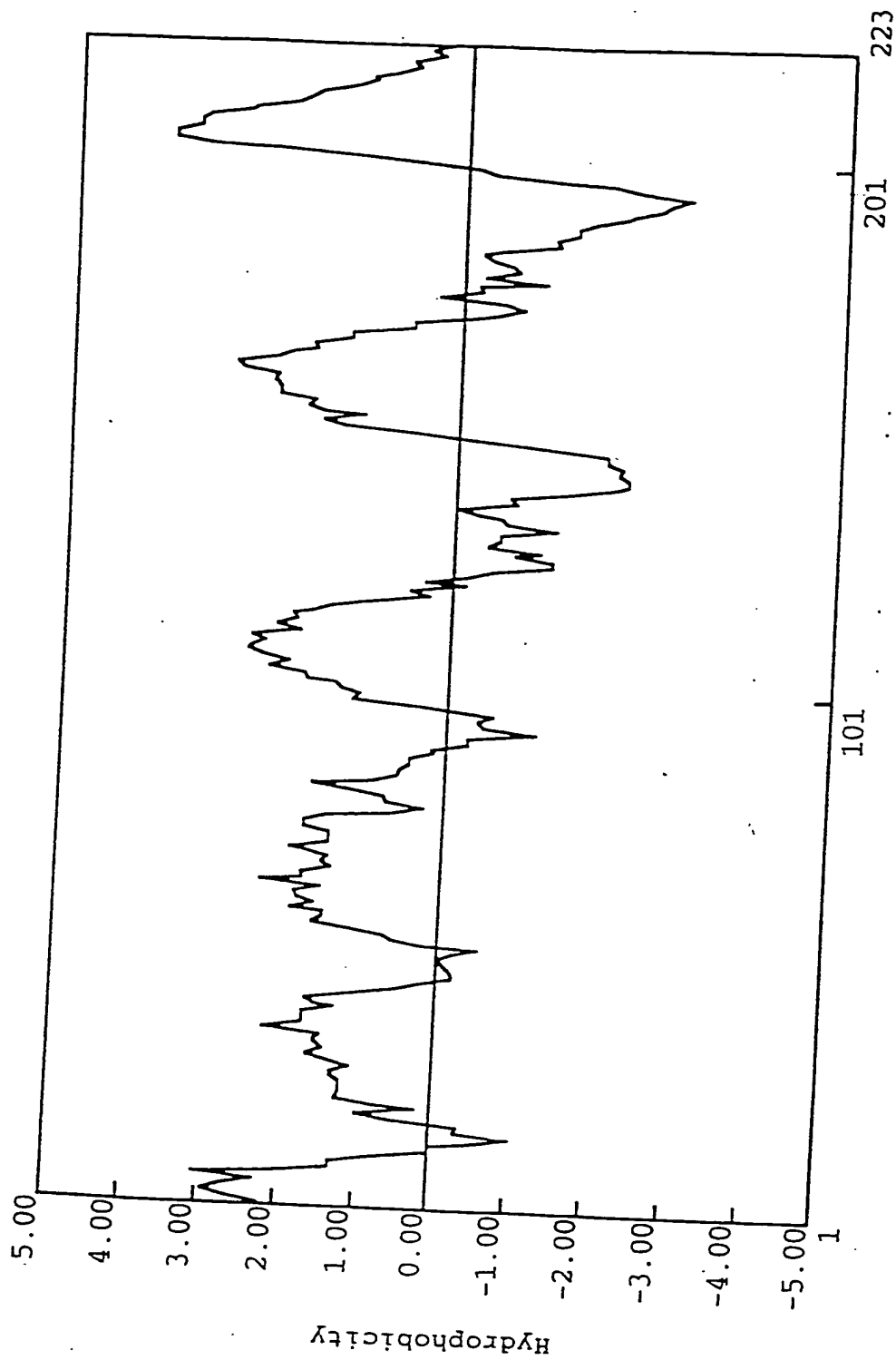
Fig. 6

5'	GTG	GGC	ATG	GTG	GGC	AAC	ATC	CTG	CTG	GTG	CTG	GTG	ATC	GCG	CGG	GTG	CGC	CGG
	Val	Gly	Met	Val	Gly	Asn	Ile	Leu	Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg
	CTG	TAC	AAC	GTG	ACG	AAT	TTC	CTC	ATC	GGC	AAC	CTG	GCC	TTG	TCC	GAC	GTG	CTC
	Leu	Tyr	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu
	ATG	TGC	ACC	GCC	TGC	GTG	CCG	CTC	ACG	CTG	GCC	TAT	GCC	TTC	GAG	CCA	CGC	GGC
	Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly
	TGG	GTG	TTC	GGC	GGC	GGC	CTG	TGC	CAC	CTG	GTC	TTC	TTC	CTG	CAG	GCG	GTC	ACC
	Trp	Val	Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Ala	Val	Thr
	GTC	TAT	GTG	TCG	GTG	TTC	ACG	CTC	ACC	ACC	ATC	GCA	GTG	GAC	CGC	TAC	GTC	GTG
	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val
	CTG	GTG	CAC	CCG	CTG	AGG	CGG	CGC	ATC	TGC	CTG	CGC	CTC	AGC	GCC	TAC	GCT	GTG
	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val
	CTG	GCC	ATC	TGG	GTG	CTG	TCC	GCG	GTG	CTG	GCG	CTG	CCC	GCC	GCC	GTG	CAC	ACC
	Leu	Ala	Ile	Trp	Val	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr
	TAT	CAC	GTG	GAG	CTC	AAG	CCG	CAC	GAC	GTG	CGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC
	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly
	TCC	CAG	GAG	CGC	CAG	CGC	CAG	CTC	TAC	GCC	TGG	GCG	CTG	CTG	CTG	GTC	ACC	TAC
	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr
	CTG	CTC	CCT	CTG	CTG	GTC	ATC	CTC	CTG	TCT	TAC	GCC	CGG	GTG	TCA	GTG	AAG	CTC
	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val	Ser	Val	Lys	Leu
	CGC	AAC	CGC	GTG	GTG	CCG	GGC	CGC	GTG	ACC	CAG	AGC	CAG	GCC	GAC	TGG	GAC	CGC
	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg
	GCT	CGG	CGC	CGG	CGC	ACC	TTC	TGC	TTG	CTG	GTG	GTG	GTC	GTG	GTG	GTG	TTC	ACC
	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr
	CTC	TGC	TGG	CTG	CCC	TTC	TTC											
	Leu	Cys	Trp	Leu	Pro	Phe	Phe											

Fig. 7

p19P2	1	10	20	30	40	50	
pG3-2/pG1-10	1	VGMVGNLLV	LVIAVRRLH	NVTNFIIGNL	ALSDVLMCTA	CVPLTLAYAF	50
	1	VGMVGNLLV	LVIAVRRLY	NVTNFIIGNL	ALSDVLMCTA	CVPLTLAYAF	50
p19P2	51	60	70	80	90	100	
pG3-2/pG1-10	51	EPRGWFVGGG	LCHLVFFLQ	VTVVSVFTL	TTIAVDRYVV	LHPLRRRI	100
	51	EPRGWFVGGG	LCHLVFFLQA	VTVVSVFTL	TTIAVDRYVV	LHPLRRRI	100
p19P2	101	110	120	130	140	150	
pG3-2/pG1-10	101	LRLSAYAVLA	IWL SAVLAL	PAAVHTYHVE	LKPHDVLCE	EFWGSQERQR	150
	151	160	170	180	190	200	
p19P2	151	GLLLV	TYLLPLLVL	LSYVRVSVKL	RNRVVPGRVT	QSQADWDRAR	200
pG3-2/pG1-10	151	QLYAWGLLLV	TYLLPLLVL	LSYVRVSVKL	RNRVVPGRVT	QSQADWDRAR	200
p19P2	201	210	220	230	240	250	
pG3-2/pG1-10	201	RRRTFCLLV	VVVFALCWL	PYY			250
	201	RRRTFCLLV	VVVFILCWL	PFF			250

Fig. 8



Position in the amino acid sequence

Fig. 9

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG	120
1		1
	Met	
121	GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACTCCCGCCAACCAGAGCGCAGAGGCCTCGGCGGGCAACGGGTGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCCGTACGCCCCCTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGTGCTCTACAGCGTCTGGTGGTCTGGGGCTGGTGGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGTATCGCGGGGTGCGCGGCTGCACAACGTGACGAACCTTCCTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCCGACGTGCTCATGTGCACCGCTGCGTGGCGCTCACGCTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTGAGCCACGCGGCTGGGTGTTCGGCGGGCGGCTGTGCCACCTGGTCTTCTTCCTGCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCACCGTCTATGTGTGCGGTGTTACGCTCACCACCATCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
501	GTGCTGGTGACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
561	GCCATCTGGGCGCTGTCCGCGGTGCTGGCGCTGCCGCGCGCGCTGCACACCTATCAGTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGCAACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCTGGGGGTGCTGTGCTGGTCACTACCTGCTCCCTCTGCTGGTCAATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCTGTCTTACGTCCGGGTGTCAGTGAAGCTCCGCAACCGGTGGTGGCGGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCGCGGCACCTTCTGCTTGCTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCTGGTGGTGTTCGCGCTGCTGGCTGCCGCTGCACGTCTTCAACCTGCTGCGG	1020
281	ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCCCTACGCCTTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTGGGCTGCTACAACCCCTTCATCTACGCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAACTGTTGGTGGCTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle...	371
1261	TCCACTTCAACTGGCCTCTAGGGCACCCTCGAGGTCAATCTGGTGTCTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

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Fig. 10

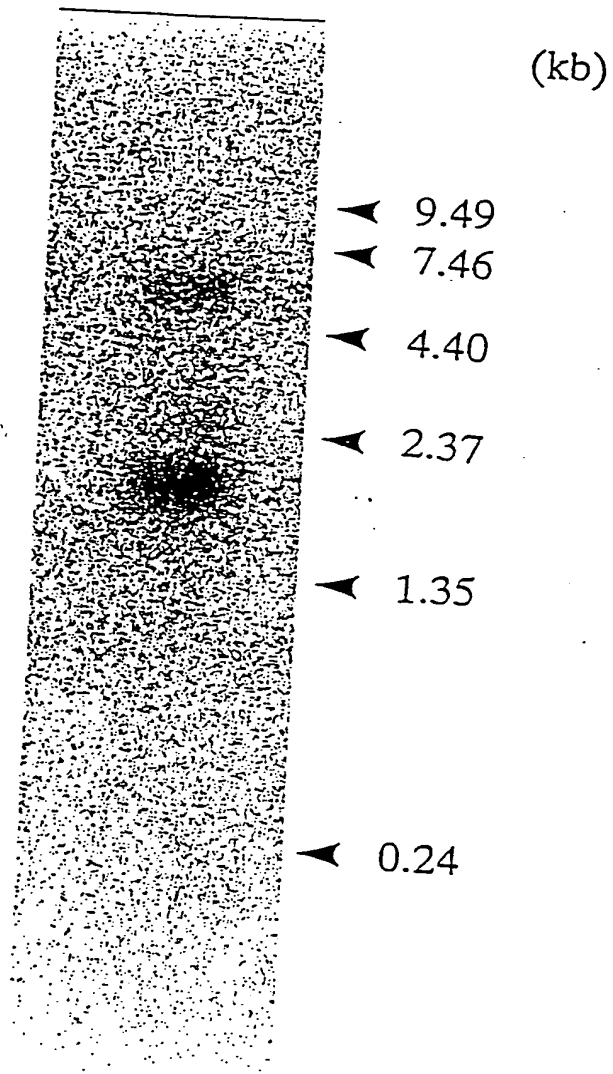


Fig. 11

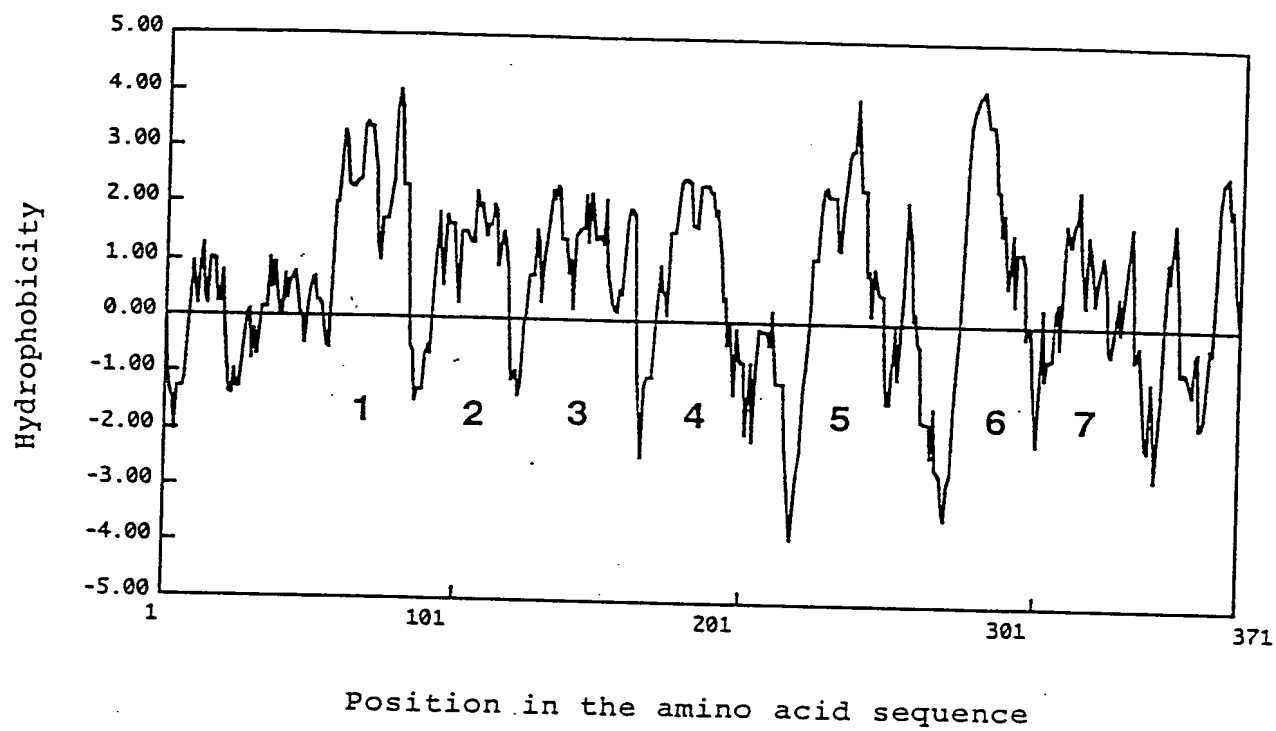


Fig. 12

5'	CTG	TGT	GTC	ATC	GCG	GTG	GAT	AGG	TAC	GTG	GTT	CTG	GTG	CAC	CCG	CTA	CGT	CGG	54
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	
	CGC	ATT	TCA	CTG	AGG	CTC	AGC	GCC	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	TCT	108
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	
	GCA	GTG	CTG	GCG	CTG	CCG	GCC	GCG	GTG	CAC	ACC	TAC	CAT	GTG	GAG	CTC	AAG	CCC	162
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	
	CAC	GAC	GTG	AGC	CTC	TGC	GAG	GAG	TTC	TGG	GGC	TCG	CAG	GAG	CGC	CAA	CGC	CAG	216
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	
	ATC	TAC	GCC	TGG	GGG	CTG	CTT	CTG	GGC	ACC	TAT	TTG	CTC	CCC	CTG	CTG	GCC	ATC	270
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile	
	CTC	CTG	TCT	TAC	GTA	CGG	GTG	TCA	GTG	AAG	CTG	AGG	AAC	CGC	GTG	GTG	CCT	GGC	324
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	
	AGC	GTG	ACC	CAG	AGT	CAA	GCT	GAC	TGG	GAC	CGA	GCG	CGT	CGC	CGC	CGC	ACT	TTC	378
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	
	TGT	CTG	CTG	GTG	GTG	GTG	GTG	GTA	GTG	TTC	ACG	CTC	TGC	TGG	CTG	CCC	TTC	TAC	432
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr	

CT 3'

Fig. 13

p19P2	1	10	20	30	40	50
PG3-2/pG1-10	1	VGWVGNVLLV	LVIAVRRLH	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF
p5S38	-79	VGWVGNVLLV	LVIAVRRLY	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF
						-30
p19P2	51	60	70	80	90	100
PG3-2/pG1-10	51	EPRGMVFGGG	LCHLVFFLQP	VTVVSVFTL	TTIAVDRYVV	LVHPLRRRI-
p5S38	-29	EPRGMVFGGG	LCHLVFFLQA	VTVVSVFTL	TTIAVDRYVV	LVHPLRRRIIS
					CVIAVDRYVV	LVHPLRRRIIS
						21
p19P2	101	110	120	130	140	150
PG3-2/pG1-10	101	LRLSAYAVLA	IWL SAVLAL	PAAVHTYHVE	LKPHDVRLCE	EFWGSQERQR
p5S38	22	LRLSAYAVLG	IWL SAVLAL	PAAVHTYHVE	LKPHDVSLCE	EFWGSQERQR
						71
p19P2	151	160	170	180	190	200
PG3-2/pG1-10	151	QLYAWGLLLV	TYLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSQADWDRAR
p5S38	72	QIYAWGLLLG	TYLLPLLAII	LSYVRVSVKL	RNRVVPGRVT	QSQADWDRAR
					RNRVVPGRVT	QSQADWDRAR
						121
p19P2	201	210	220	230	240	250
PG3-2/pG1-10	201	RRRTFCLLVV	VWVFALCWL	PYN		
p5S38	122	RRRTFCLLVV	VWVFALCWL	PFE		
						250
						250
						171

Fig. 14

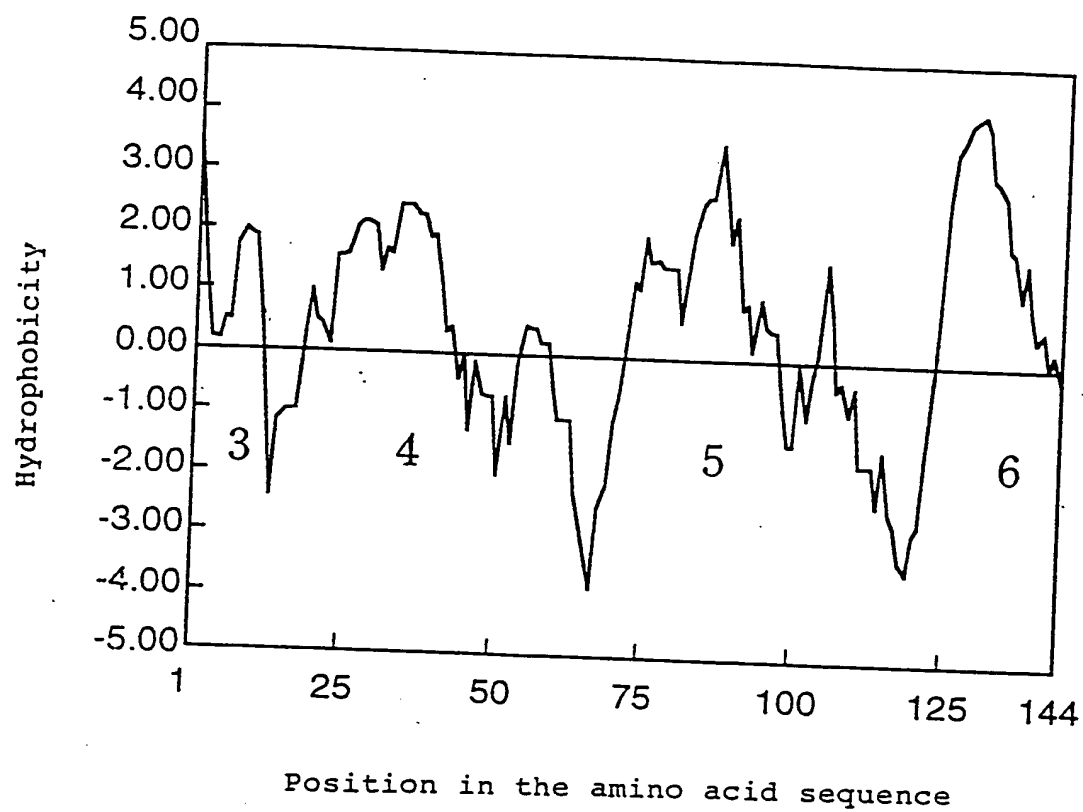


Fig. 15

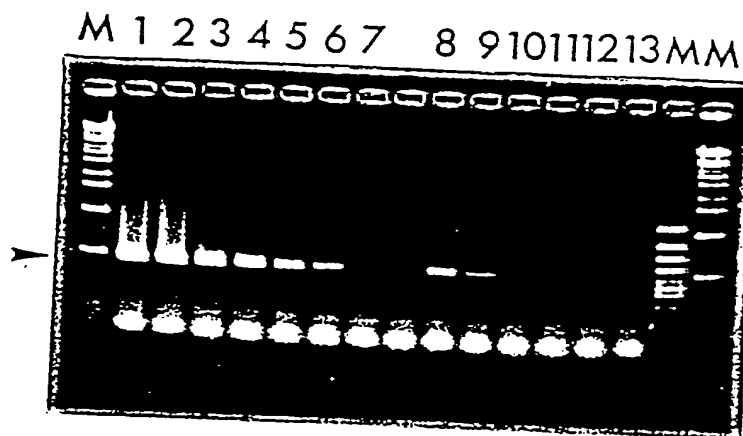
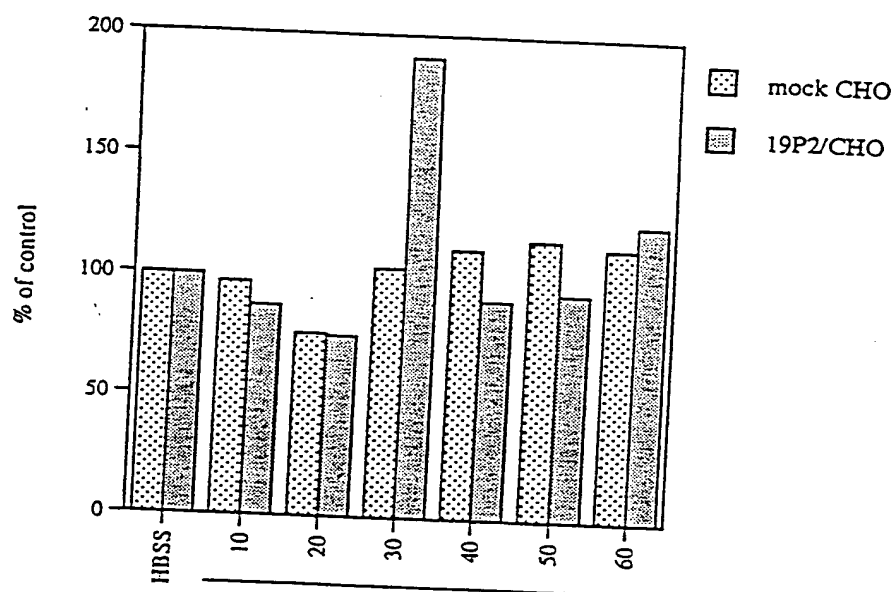


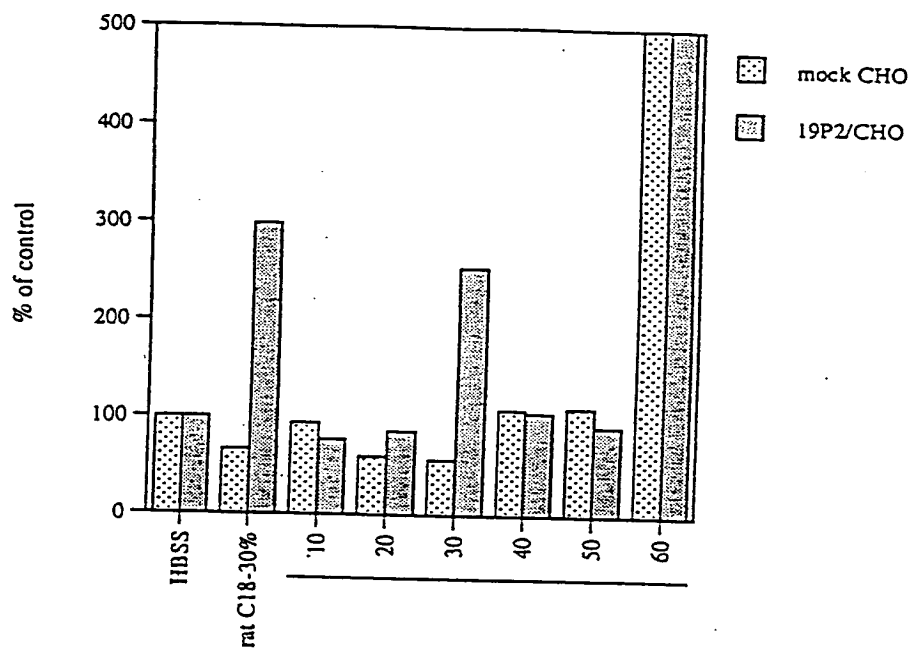
Fig. 16



rat whole brain extract

C₁₈-column CH₃CN elution (%)

Fig. 17



bovine hypothalamus extract

C₁₈-column CH₃CN elution (%)

Fig. 18

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Fig. 19

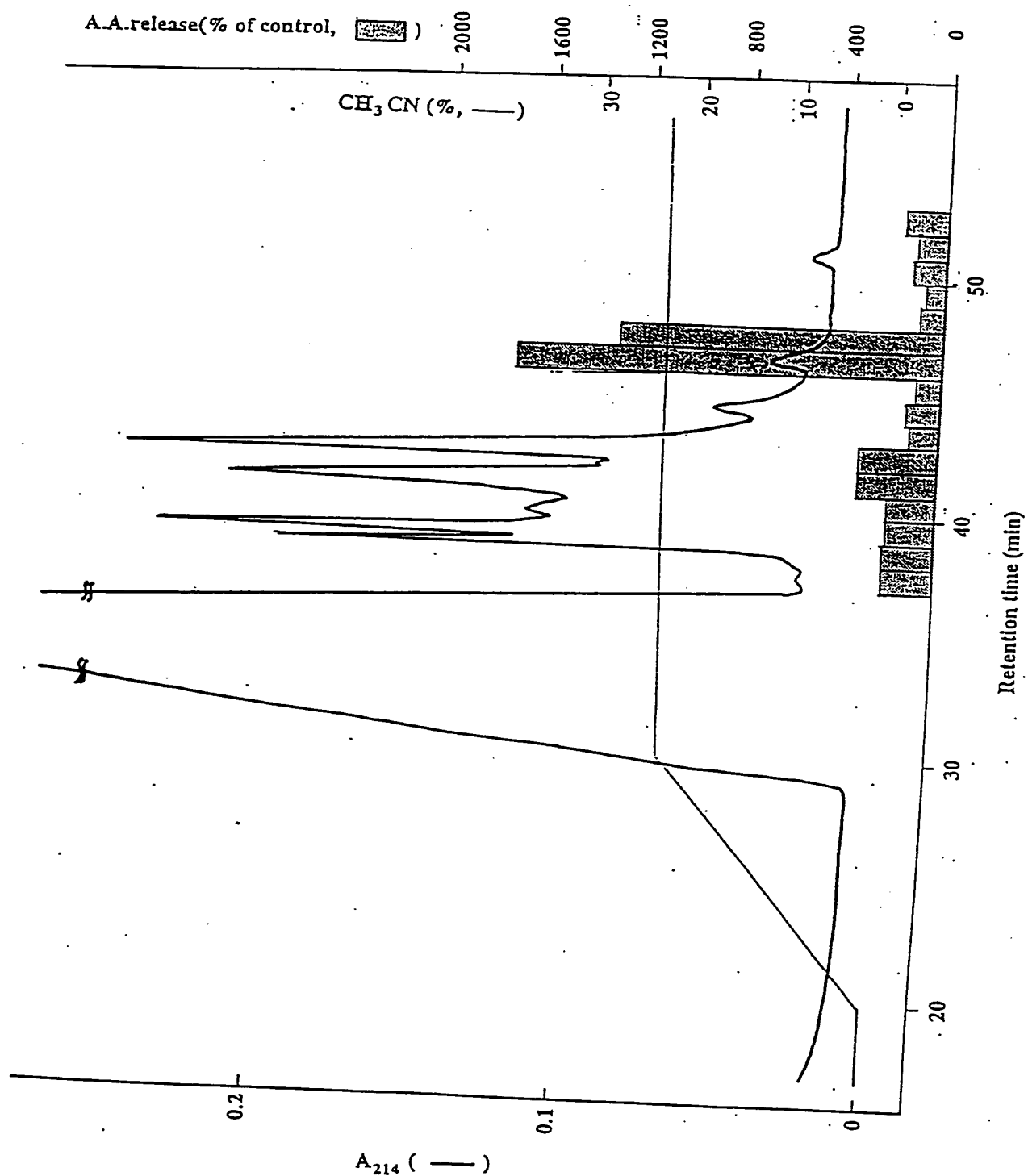


Fig. 20

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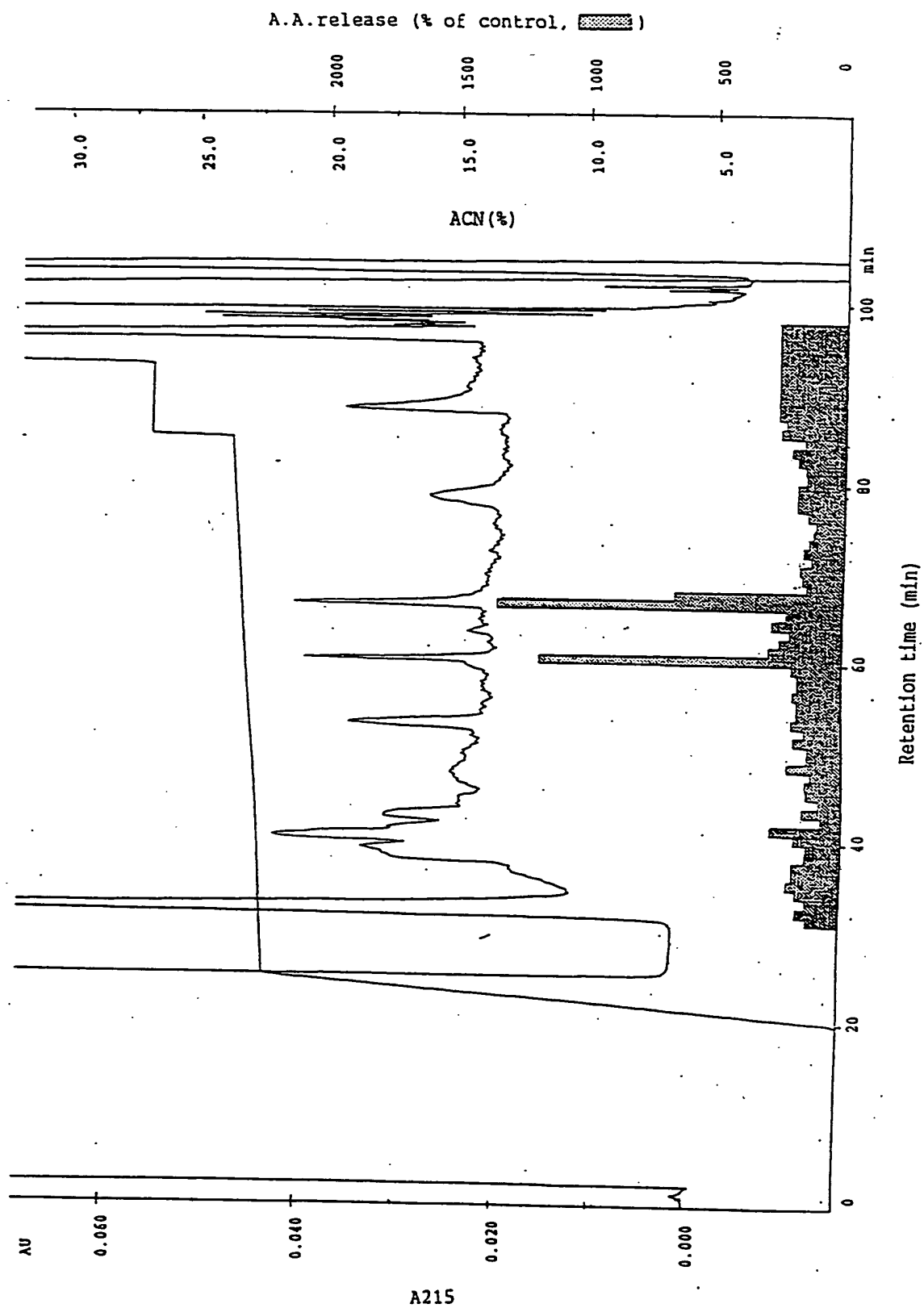


Fig. 21

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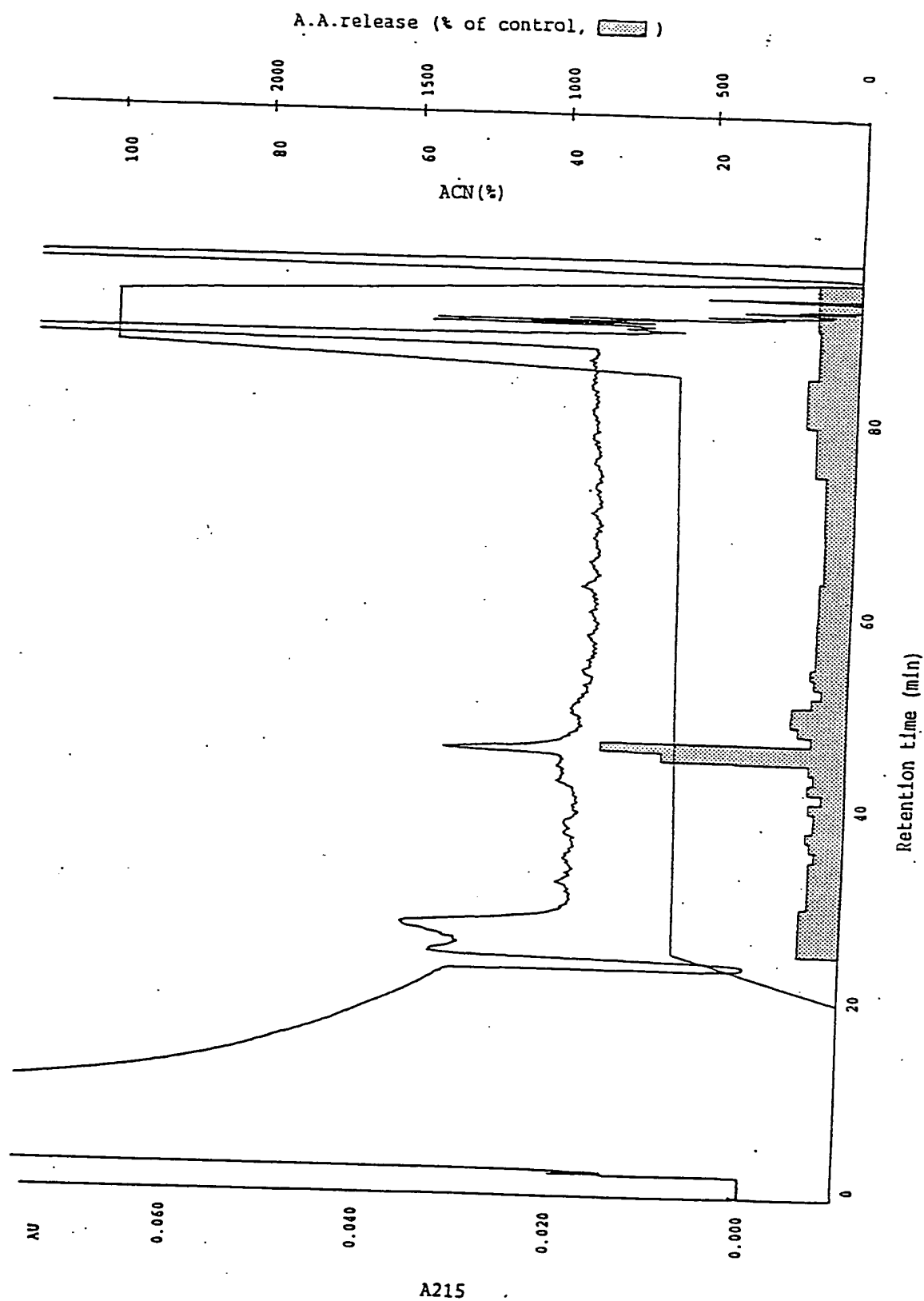


Fig. 22

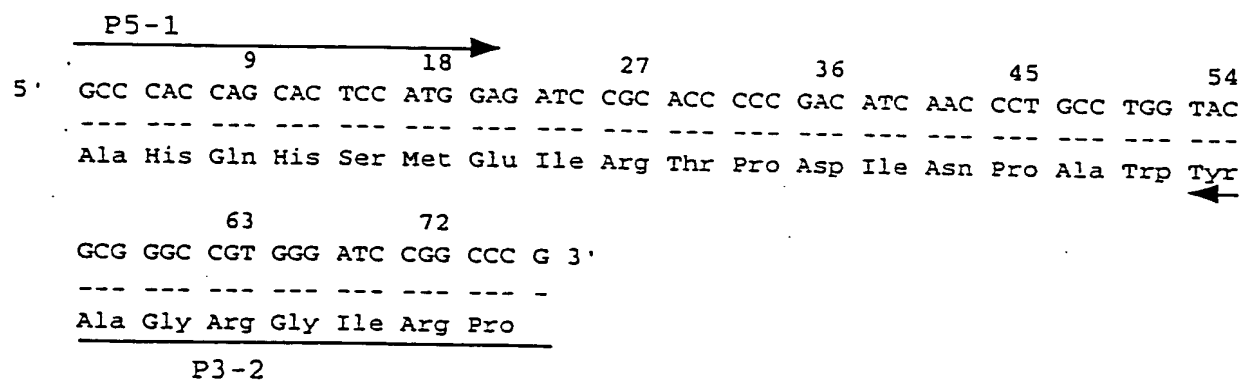


Fig. 23

1	GTGGAATGAAGGCGGTGGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
	← PDN	
120	CCTGCCT	126
39	<u>ProAla</u>	40

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Fig. 24(a)

1	GTGGAATGAAGGCGGTGGGGGCTGGCTCCTCTGCCTGCTGCTGCTGGGCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGGCCCGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla	58
180	GGCCCGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA	239
59	AlaProGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

Fig. 24(b)

1	GTGGAATGAAGGCGGTGGGGGCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGGCCCGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla	58
180	GCCCTGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA	239
59	AlaLeuGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCAGCCCTCCCGGGGCGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

Fig. 25

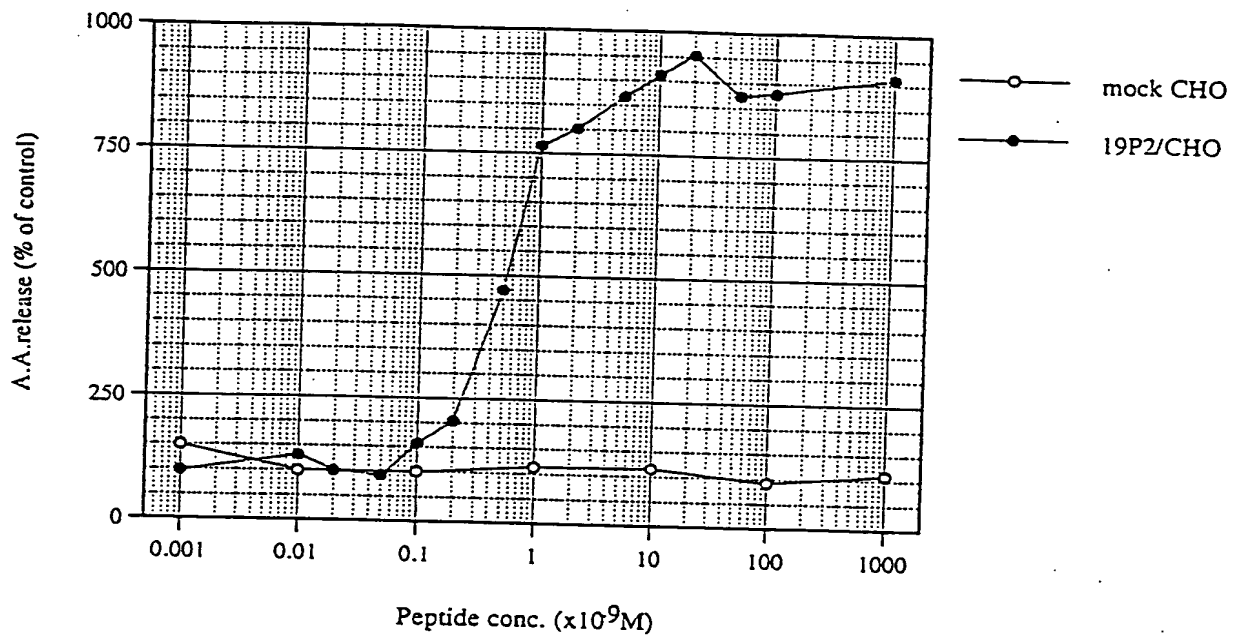


Fig. 26

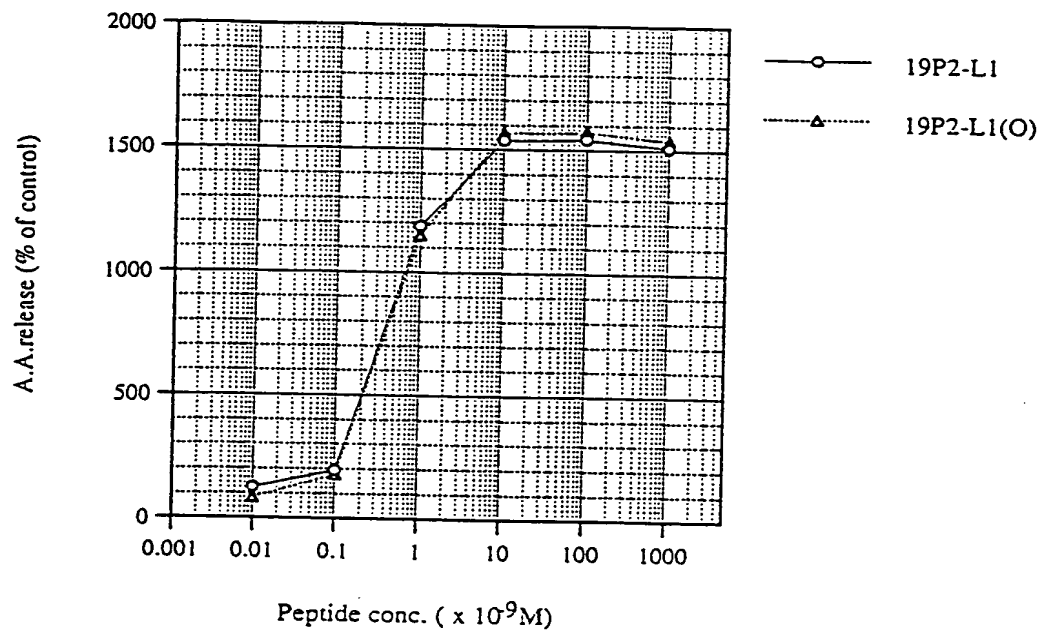


Fig. 27

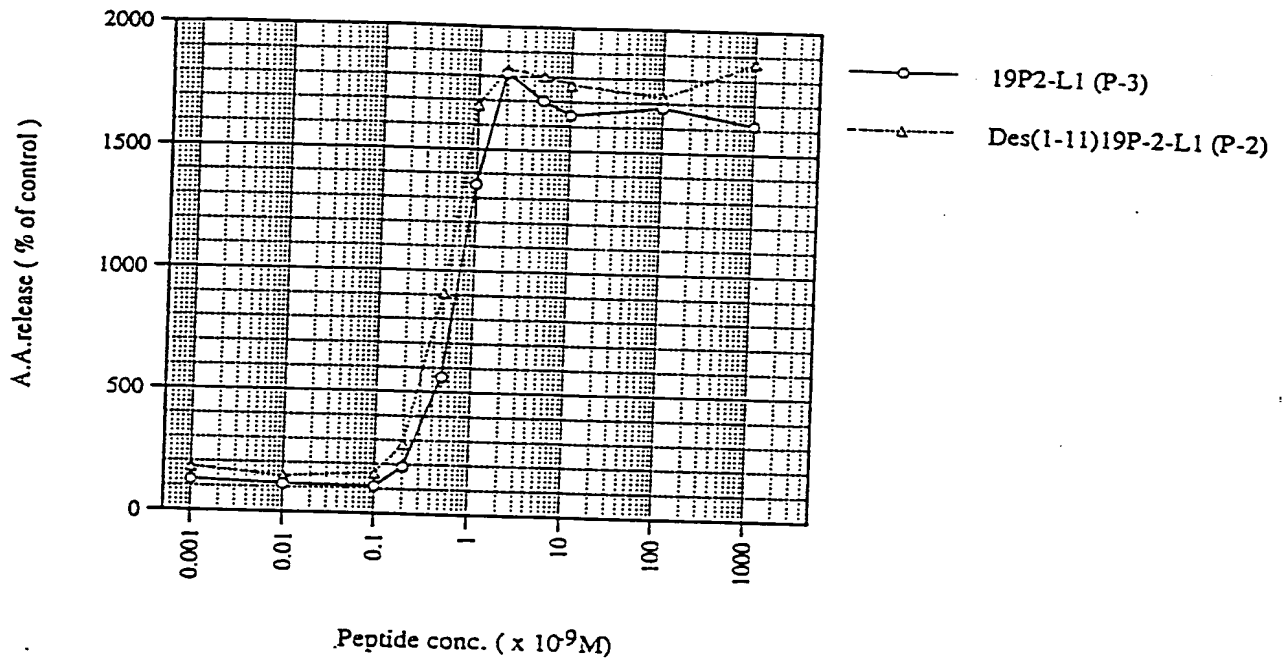


Fig. 28

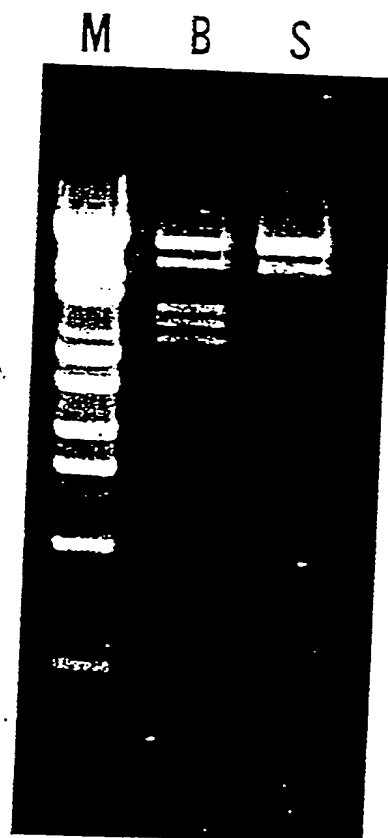


Fig. 29

10	20	30	40	50	60
ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTGTTGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.

Fig. 30

genome	10	20	30	40	50	
cDNA	1 ATGAAGGCGG	TGGGGGCGCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	50
	1 ATGAAGGCGG	TGGGGGCGCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	50
genome	60	70	80	90	100	
cDNA	51 CCTGCAGGGG	GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	100
	51 CCTGCAGGGG	GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	100
genome	110	120	130	140	150	
cDNA	101 GTGAGTGTCT	AGCCCCGCCC	CTGCCCCCAG	GGGTACACAG	GGGGGCGCTG	150
	101 -----	-----	-----	-----	-----	150
genome	160	170	180	190	200	
cDNA	151 CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	GCATCCTGGG	GTTGGGGTPT	200
	151 -----	-----	-----	-----	-----	200
genome	210	220	230	240	250	
cDNA	201 GGCTTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA	CAGGTGCTCC	250
	201 -----	-----	-----	-----	-----	250
genome	260	270	280	290	300	
cDNA	251 CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCTC	ACCACACGGG	300
	251 -----	-----	-----	-----	-----	300
genome	310	320	330	340	350	
cDNA	301 TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	350
	301 -----	-----	-----	-----	-----	350
genome	360	370	380	390	400	
cDNA	351 GGAAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	400
	351 -----	-----	-----	-----	-----	400
genome	410	420	430	440	450	
cDNA	401 AAGCCACCCC	AGCACCAGAA	ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	450
	401 -----	-----	-----	-----	-----	450
genome	460	470	480	490	500	
cDNA	451 GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	GGCAGCCATG	AGCTGAGCAC	500
	451 -----	-----	-----	-----	-----	500
genome	510	520	530	540	550	
cDNA	501 ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT	550
	501 -----	-----	-----	-----	-----	550
genome	560	570	580	590	600	
cDNA	551 GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCCTG	CCTGGTACGC	600
	551 -----	-----	-----	-----	-----	600
genome	610	620	630	640	650	
cDNA	601 AGGCCGTTGG	ATCCGGCCCCG	TGGGCGGCTT	CGGCCGGCGA	AGAGCTGCC	650
	601 GGGCCGTTGG	ATCCGGCCCCG	TGGGCGGCTT	CGGCCGGCGA	AGAGCTGCC	650
genome	660	670	680	690	700	
cDNA	651 TGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	700
	651 CGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	700
genome	710	720	730	740	750	
cDNA	701 CTGGAAGGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	750
	701 CTGGAAGGCG	GCGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	750
genome	760	770	780	790	800	
cDNA	751 CCAGCTGGTC	CAGGAATAA.	800
	751 CCAGCTGGTC	CAGGAATAA.	800

Fig. 32

1	GGCATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG	59
1	MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu	12
60	CTAAGCTTGGTCCTCCCAGGGGCTTCCAGCCGAGCCCACCAGCACTCCATGGAGACAAGA	119
13	LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg	32
120	ACCCCTGATATCAATCCTGCCTGGTACACGGGCGCGGGATCAGGCCTGTGGGCCGCTTC	179
33	ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe	52
180	GGCAGGAGAAGGGCAACCCCGAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA	239
53	GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro	72
240	CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCCAGCTCGAGAAGACAGTGC	299
73	LeuAspGlyArgThrLysPheSerGlnArgGly***	83
300	TGCTGAGCCCAAGCCCACACTCCCTGTCCCCTGCAGACCCTCCTCTACCCTCCCTCTCCT	359
83		83
360	CTGCT	364
83		83

bovine.aa

bovine.aa				M K A V G A W L L		
bovine.seq	-18	10	20	30	40	50
rat.seq	1	GGCATCATCC AGGAAGACGG	AGCATG---G	CCTTGAAGAC	GTGGCTTCTG	
bovine.aa		C L L L L G L A L Q G A A S R A H				
bovine.seq	33	TGCCTGCTGC TGCTGGGCCT	GGCCCTGCAG	GGGGCTGCCA	GCAGAGCCCCA	
rat.seq	51	TGCTTGCTGC TGCTAAGCTT	GGTCCTCCCA	GGGGCTTCCA	GCCGAGCCCCA	
bovine.aa		Q H S M E I R T P D I N P A W Y A				
bovine.seq	83	CCAGCACTCC ATGGAGATCC	GCACCCCAGA	CATCAACCCT	GCCTGGTACG	
rat.seq	101	CCAGCACTCC ATGGAGACAA	GAACCCCTGA	TATCAATCCT	GCCTGGTACA	
bovine.aa		G R G I R P V G R F G R R R A A				
bovine.seq	133	CGGGCCGTTGG GATCCGGGCC	GTGGGCCGCT	TGGGCCGGCG	AAGAGCTGCC	
rat.seq	151	CGGGCCGCGG GATCAGGCCT	GTGGGCCGCT	TGGGCAGGAG	AAGGGCAACC	
bovine.aa		P G D G P R P G P R R V P A C F R				
bovine.seq	183	CCGGGGGACG GACCCAGGCC	TGGCCCCCGG	CGTGTGCCGG	CCTGCTTCGG	
rat.seq	201	CCGAGGGATG TCACTGGACT	TGGC-----	---CAACTCA	GCTGCCTCCC	
bovine.aa		L E G G A E P S R A L P G R L T A				
bovine.seq	233	CCTGGAAGGC GGCGCTGAGC	CCTCCCGAGC	CCTCCCGGGG	CGGCTGACGG	
rat.seq	251	ACTGGATGGA CGCACCAAGT	TCTCTCAGCG	TGGATAACAC	CCCAGCTCGA	
bovine.aa		Q L V Q E *				
bovine.seq	283	CCCAGCTGGT CCAGGAATAA	CAGCGGGAGC	CTGCCCCCCA	CCCCTCCTCC	
rat.seq	301	GAAGACAGTG CTGCTGAGCC	CAAGCCCACA	CTCCCTGTCC	CCTGCAGACC	
bovine.aa		TCCACCAGCC ACCTTCCCTC	CAGTCTTAAT	AAAAGCAGCT	GGCTTGTT..	
bovine.seq	333	TCCACCAGCC ACCTTCCCTC	CAGTCTTAAT	AAAAGCAGCT	GGCTTGTT..	
rat.seq	351	CTCCTCTACC CTCCTCTCC	TCTGCT....			

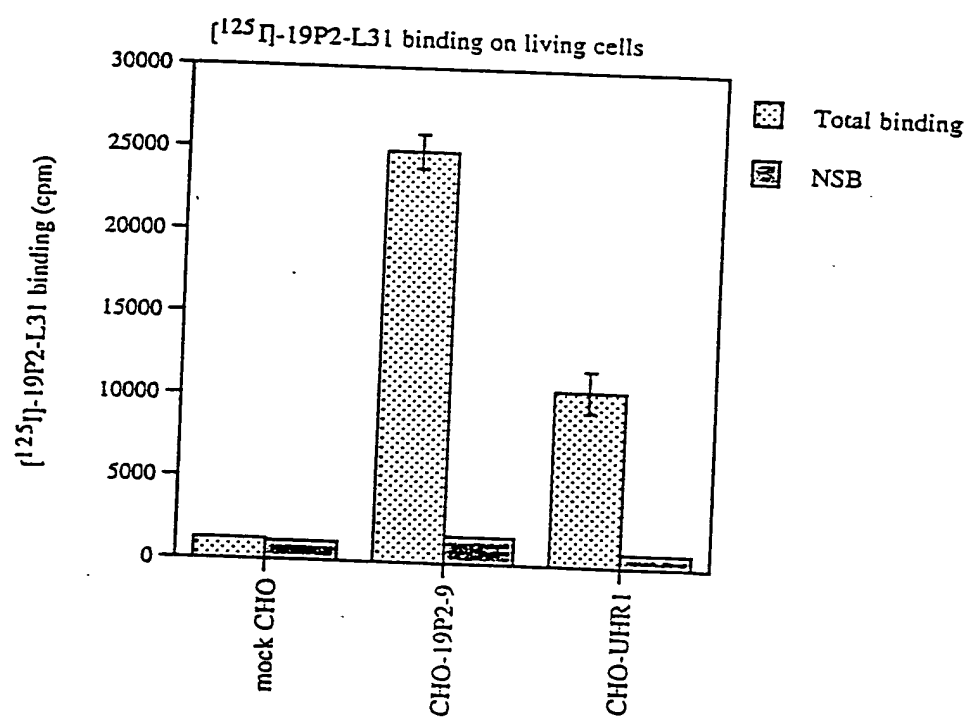
Fig. 34

1	GGCCTCCTCGGAGGAGCCAAGGGATGAAGGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG	59
1	MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu	12
60	ATGCTGGGCCTGGCCCTGCGGGGAGCTGCAAGTCGTACCCATCGGCACTCCATGGAGATC	119
13	MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle	32
120	CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCTGTGGGCGGC	179
33	ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg	52
180	TTCGGTCGGAGGAGGGCAACCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG	239
53	PheGlyArgArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu	72
240	ACCTGCTTCCCCCTGGAAGGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT	299
73	ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly***	87
300	CAAGAACTCACTCTGGAGCCTCCCCCACCACCCCTCTCCTCTCCTTCGGGCTCCTTTC	359
87		87
360	CC	361
87		87

[illegible]

		10		20		30		40		50	
bovine.aa	1	MKAVGAWLLC	LLLLGLALQG	AASRAHQHSM	EIRTPDINPA	WYAGRGIRPV					
rat.aa	1	M-ALKTWLLC	LLLLSLVLPG	ASSRAHQHSM	ETRTPDINPA	WYTGGRIRPV					50
human.aa	1	MKVLRAWLLC	LIMLGLALRG	AASRTHRHSM	EIRTPDINPA	WYASRGIRPV					50
		60		70		80		90		100	
bovine.aa	51	GFGRRRAAP	GDGFRPGPRR	VPACFRLEGG	AEPSRALPGR	LTAQLVQE*					
rat.aa	51	GFGRRRAATP	RDVIGLG---	QLSCLPLDGR	TKFSQRG*					100
human.aa	51	GFGRRRAATL	GDVFKPGLRP	RLTCFPLEGG	AMSSQDG*					100

Fig. 36



cells; 0.5×10^7 cells/ml
^[125]I]-19P2-L31; 200pM (avg. 63857.3cpm)
 NSB; 200nM (x 1,000)
 reaction; RT, 2.5hr
 in HBSS + 0.05% BSA + 0.05% CHAPS
 in 100 μ l

Fig. 37

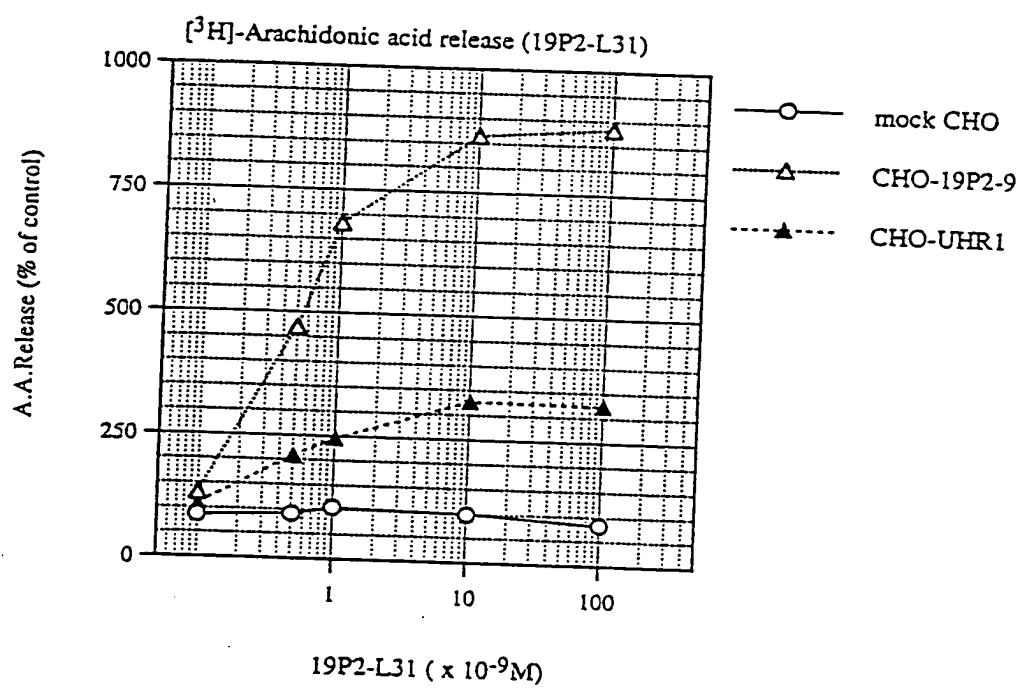


Fig. 38

UHR-1

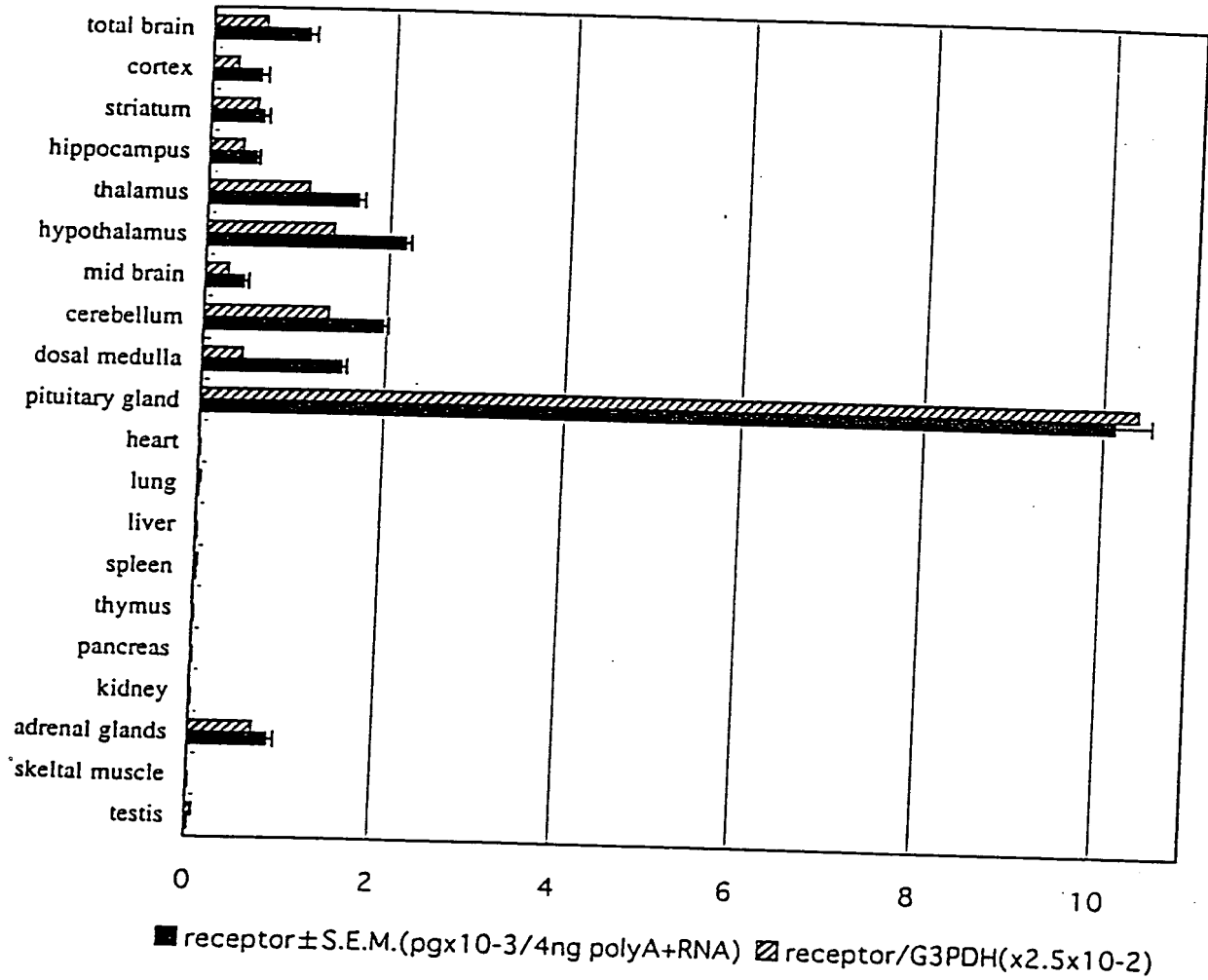


Fig. 39

ligand polypeptide

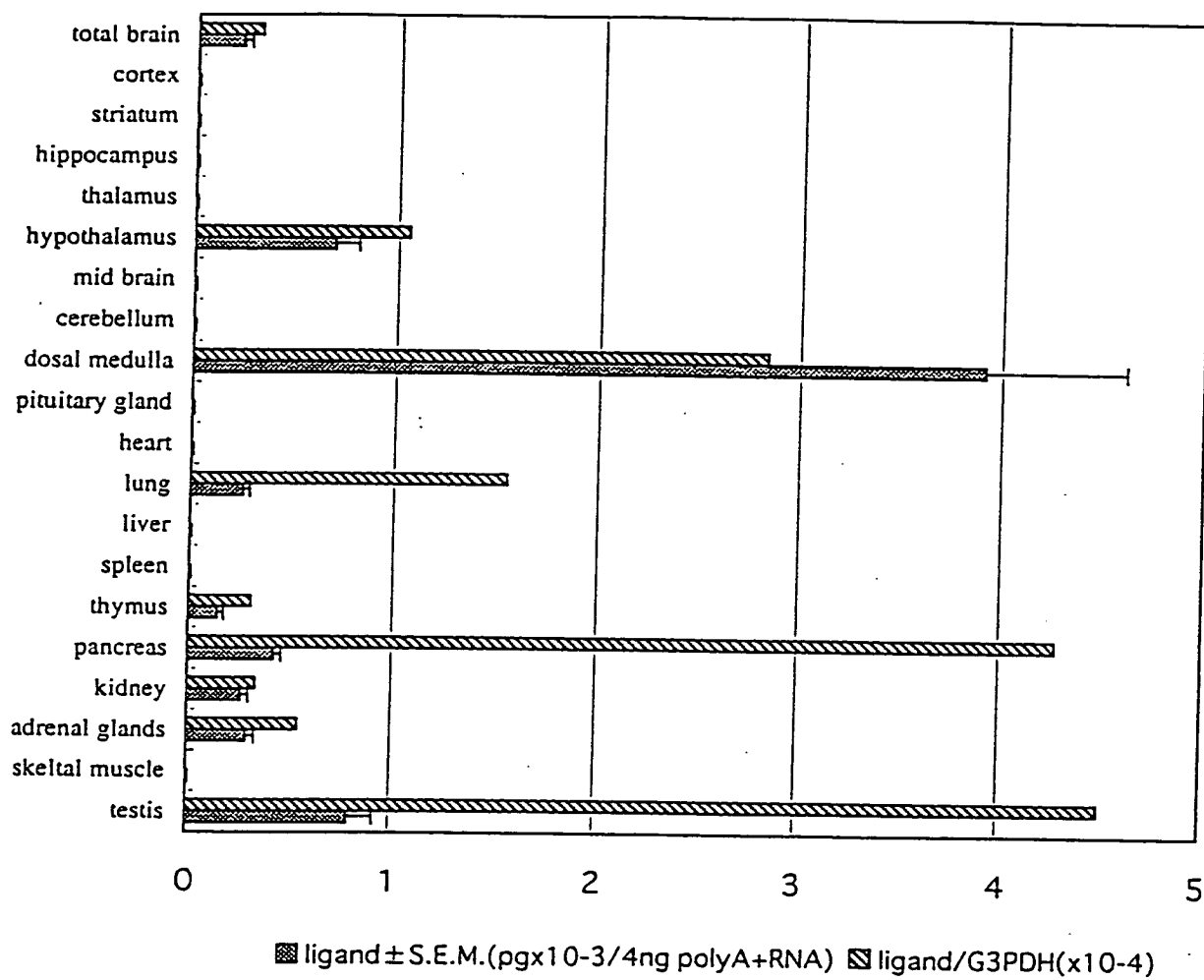


Fig. 40

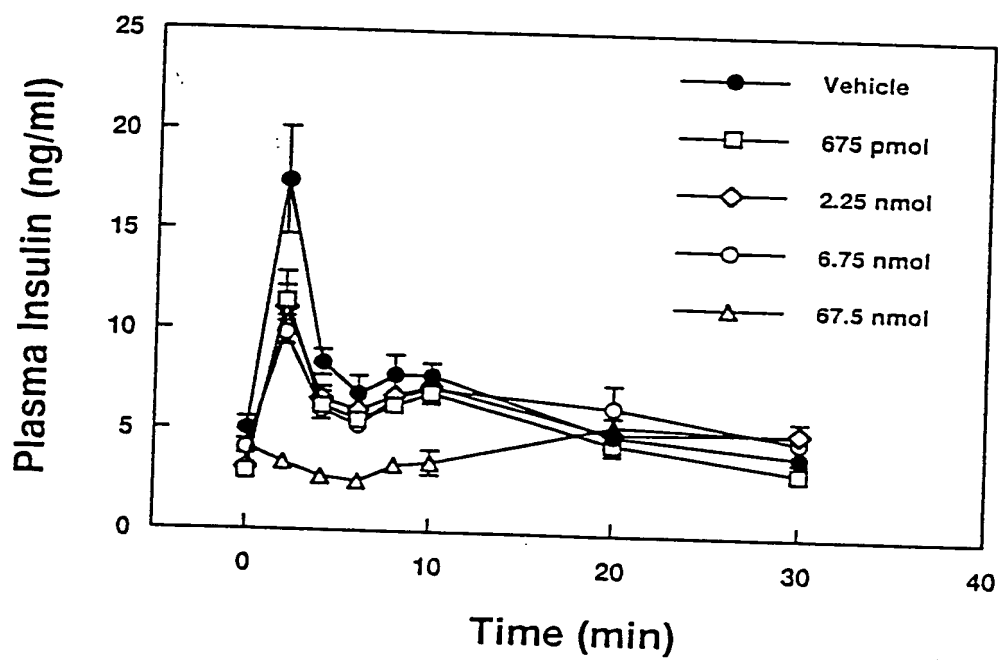
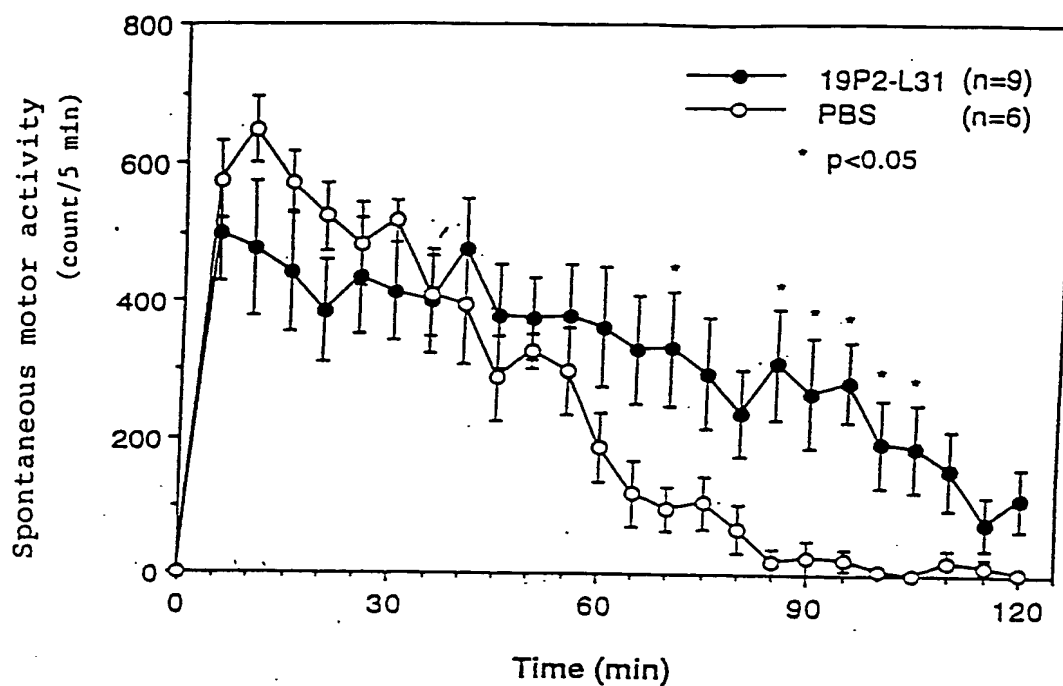


Fig. 41

(a)



(b)

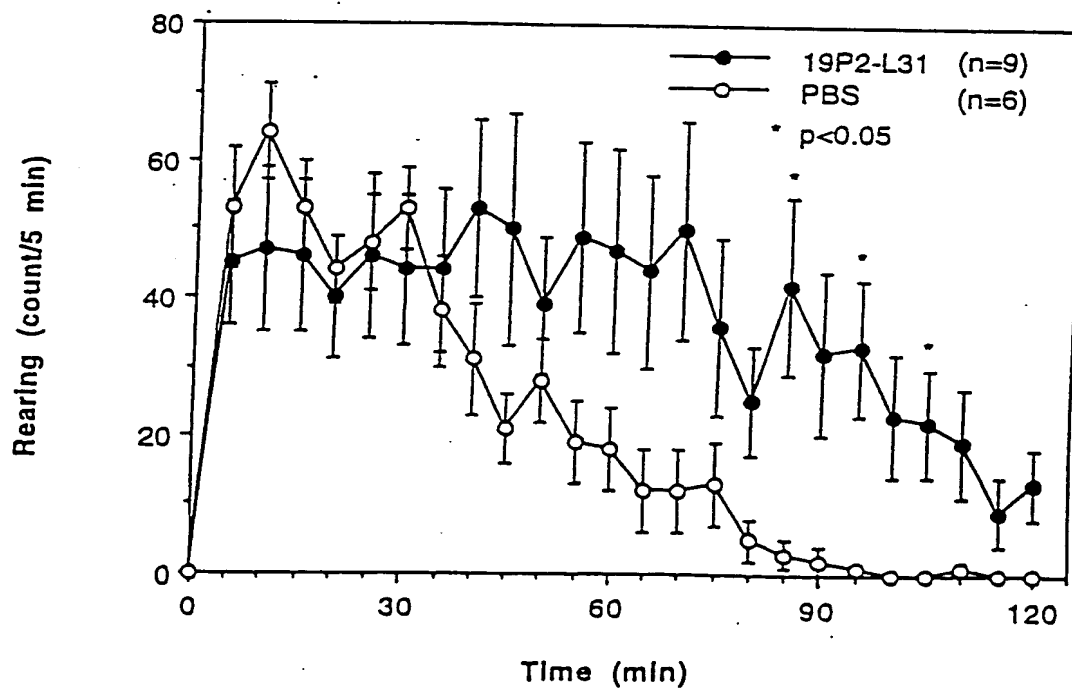
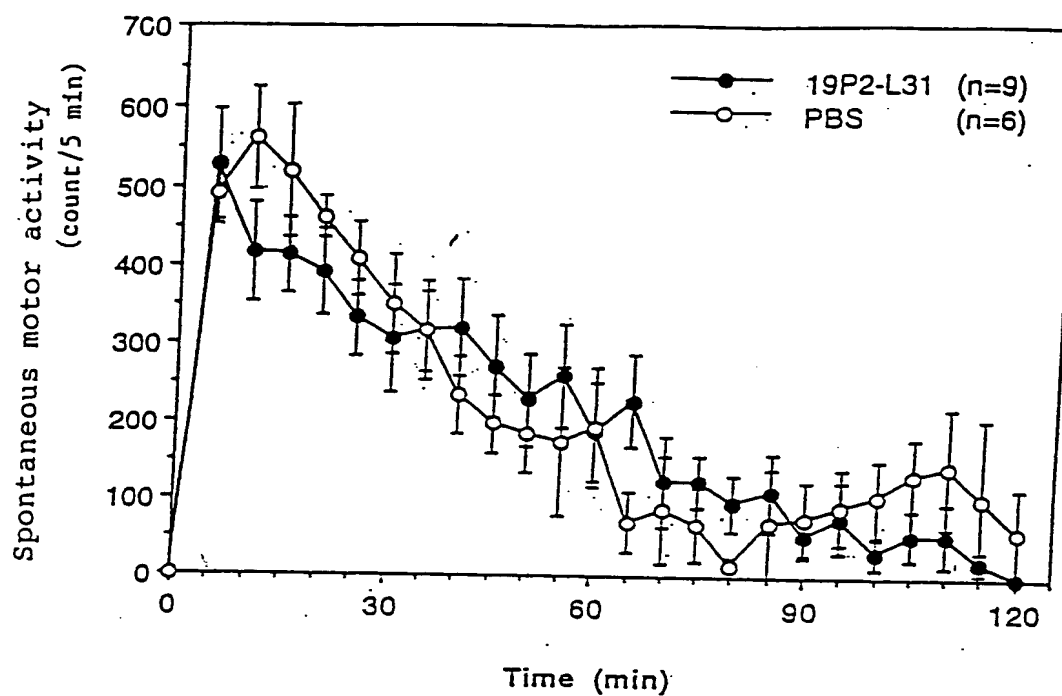


Fig. 42

(a)



(b)

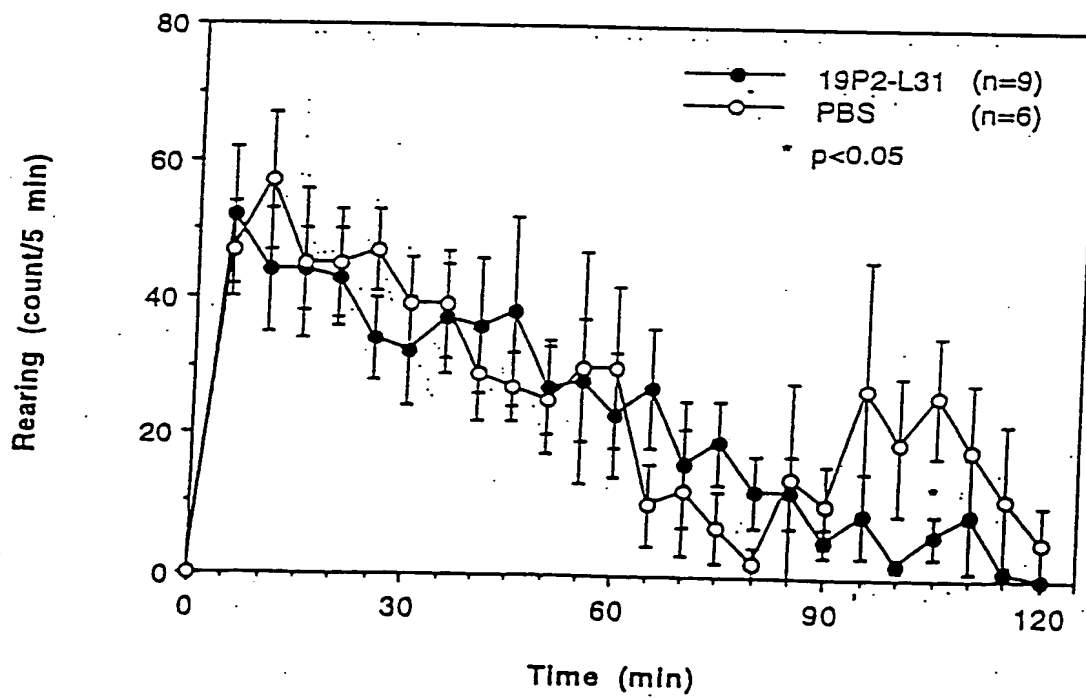
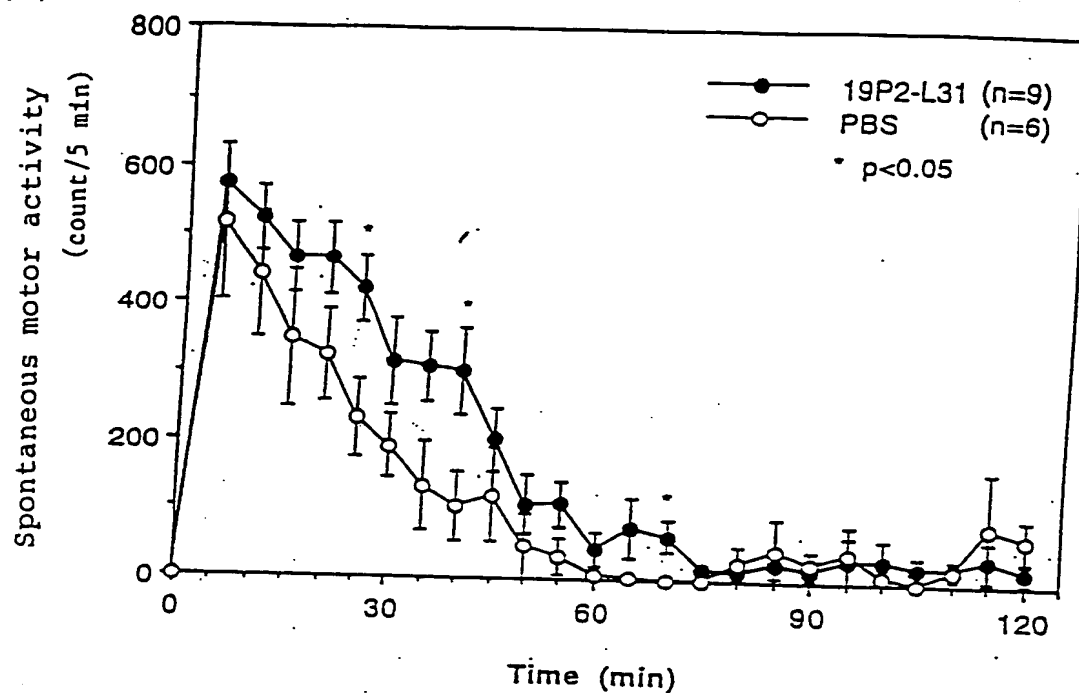


Fig. 43

(a)



(b)

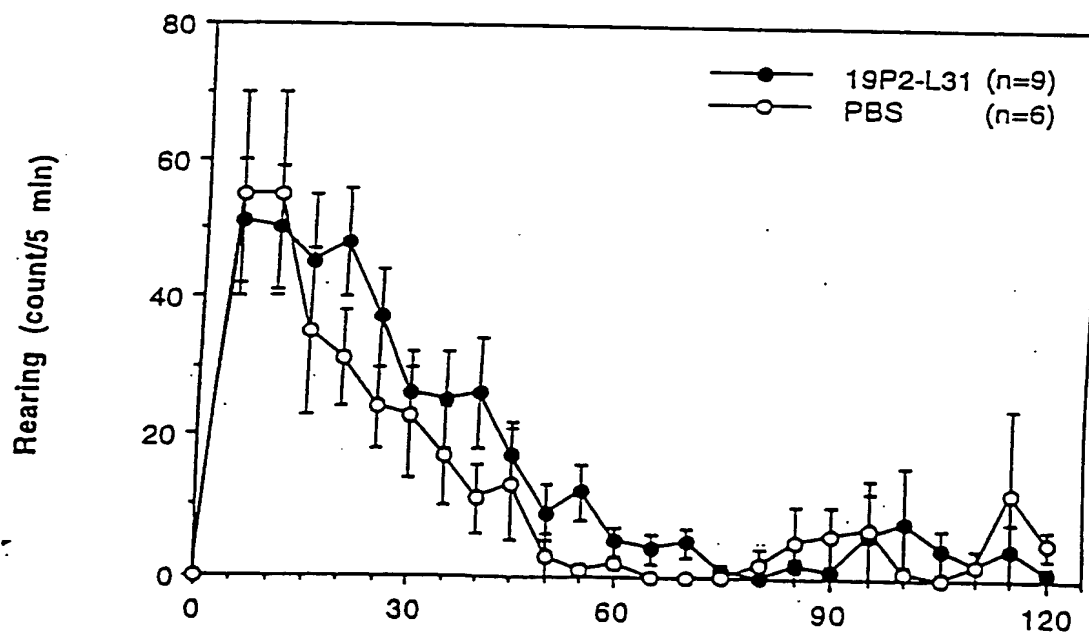
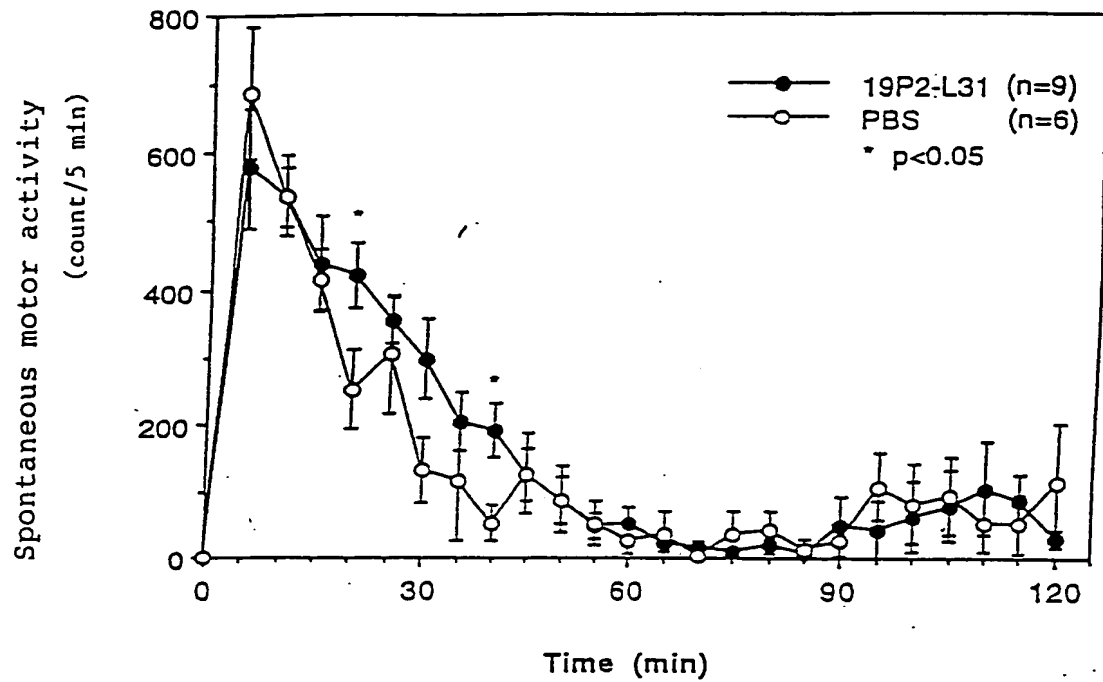


Fig. 44

(a)



(b)

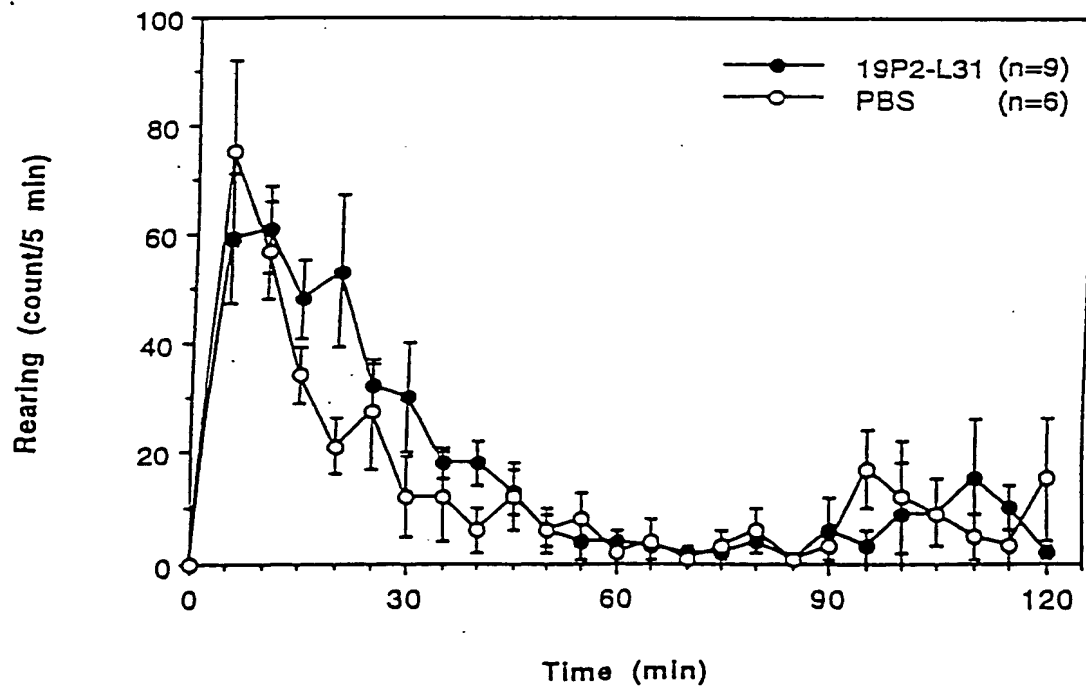


Fig. 45

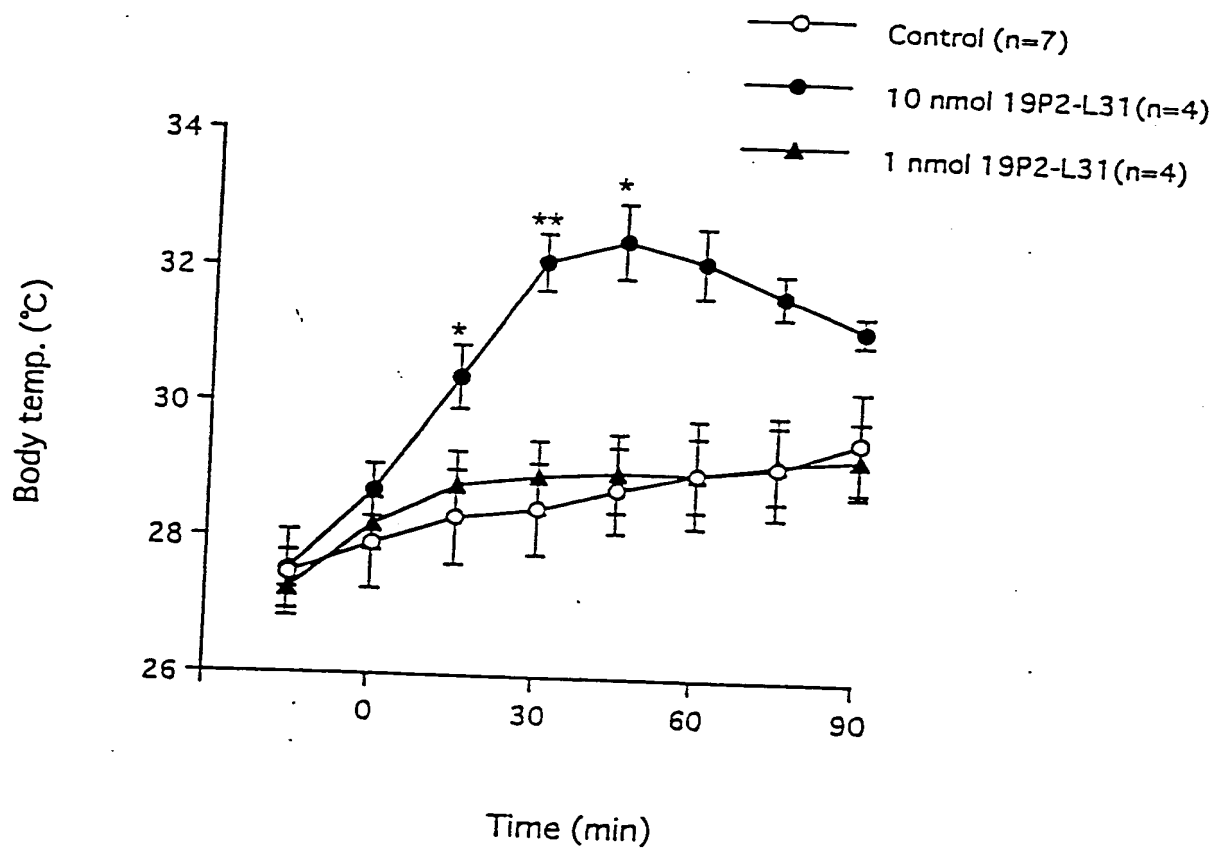
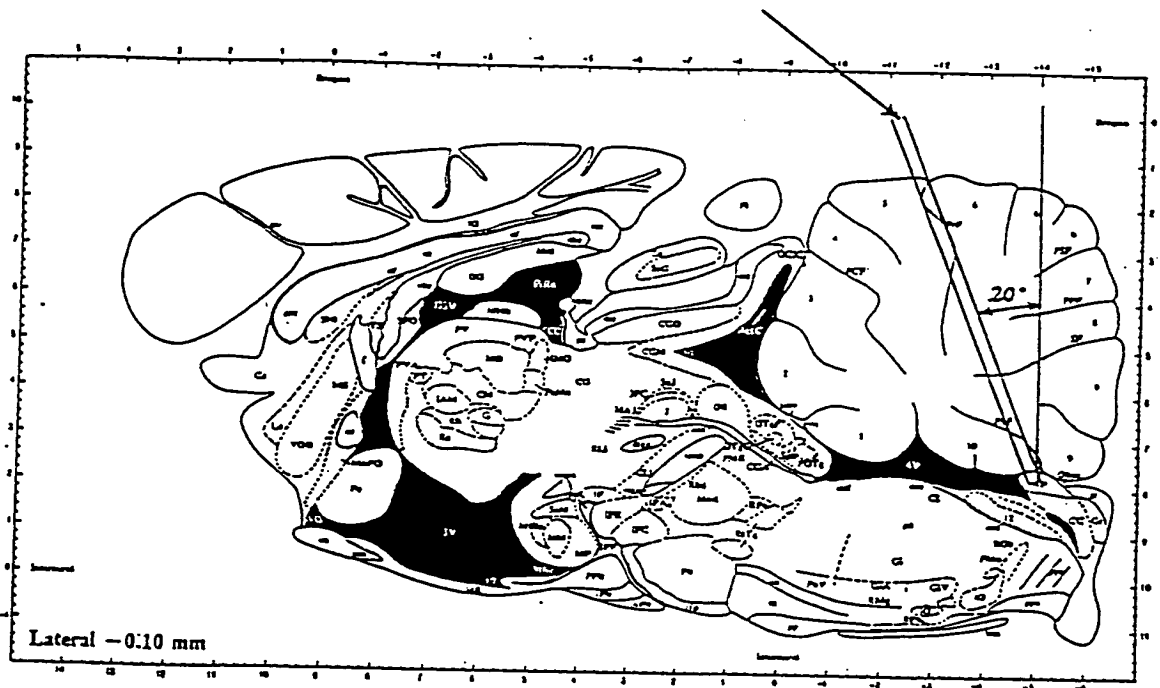
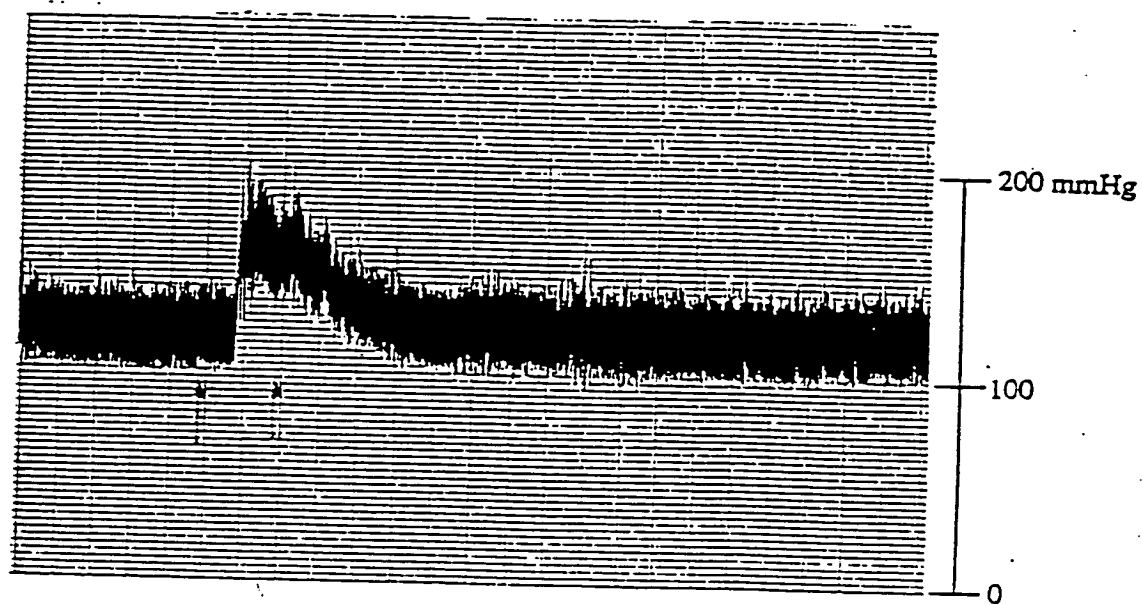


Fig. 46

micro-injection cannula



direct blood pressure



mean blood pressure

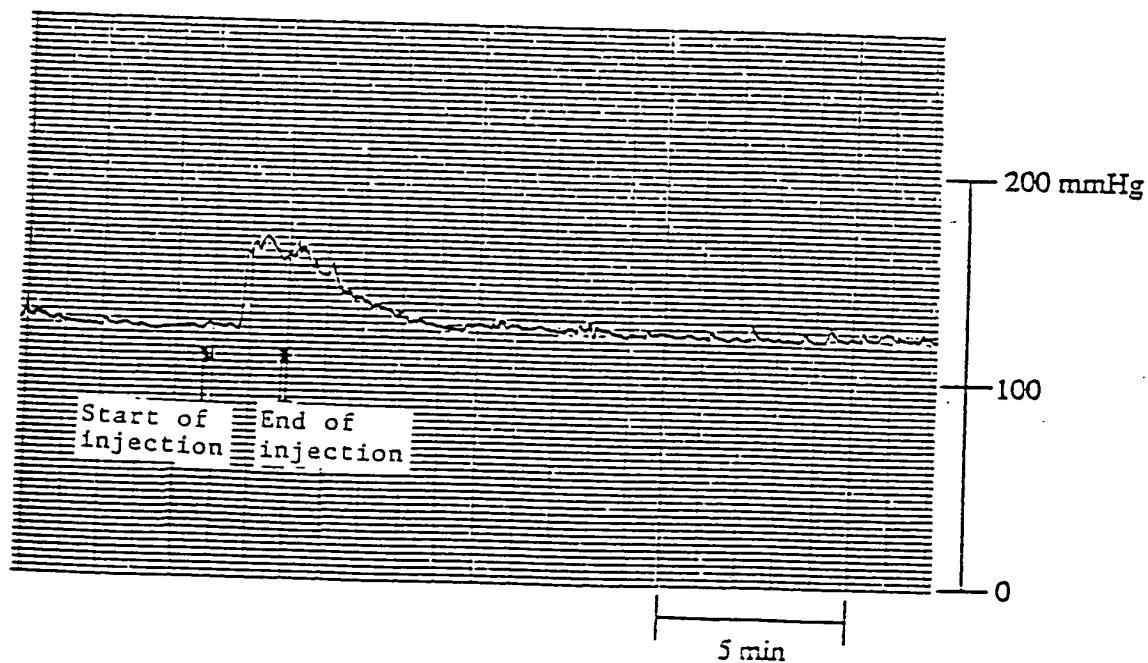


Fig. 48

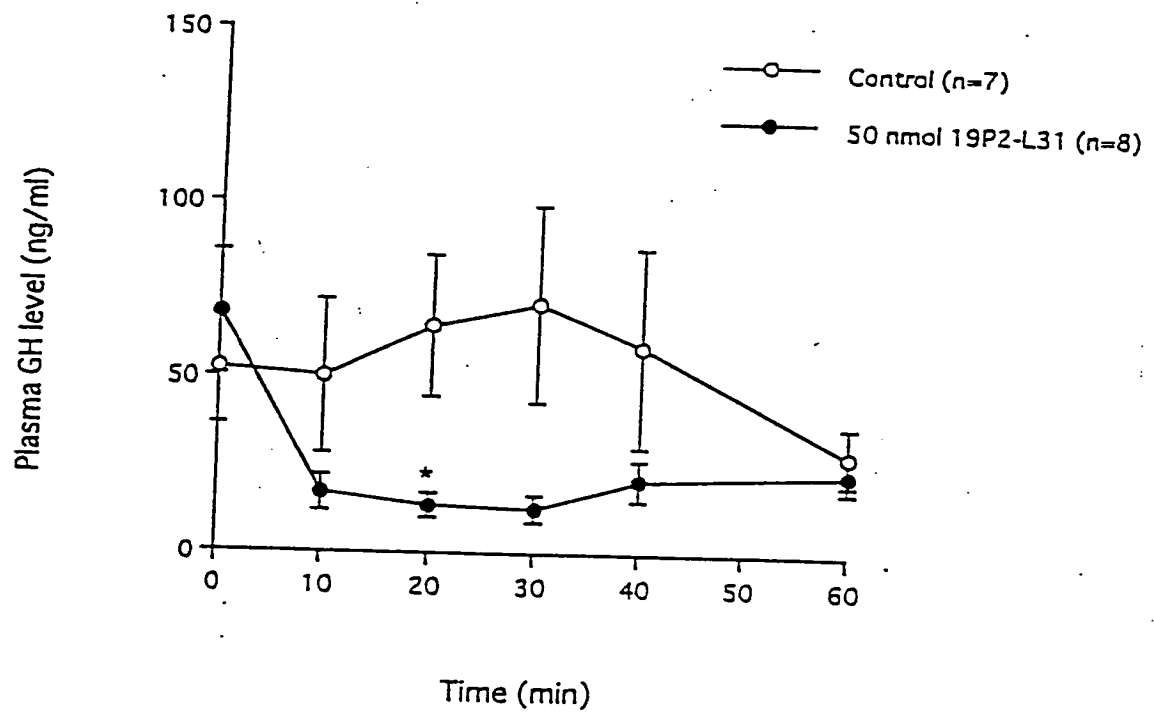


Fig. 49

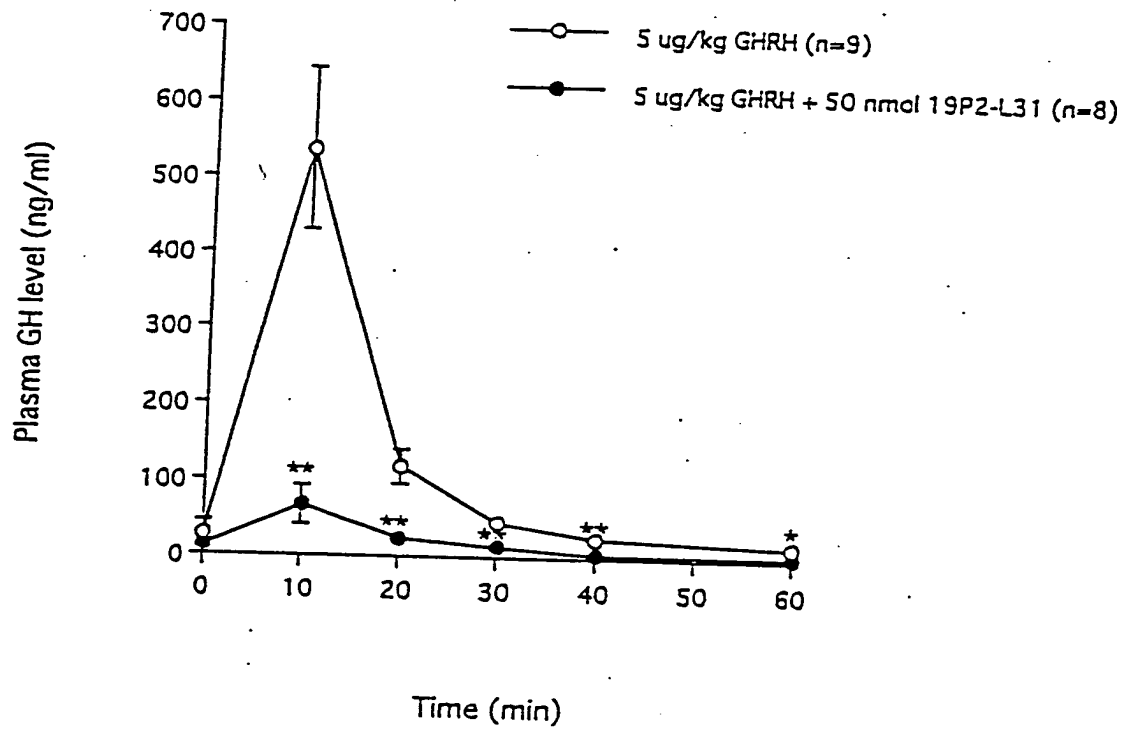


Fig. 50

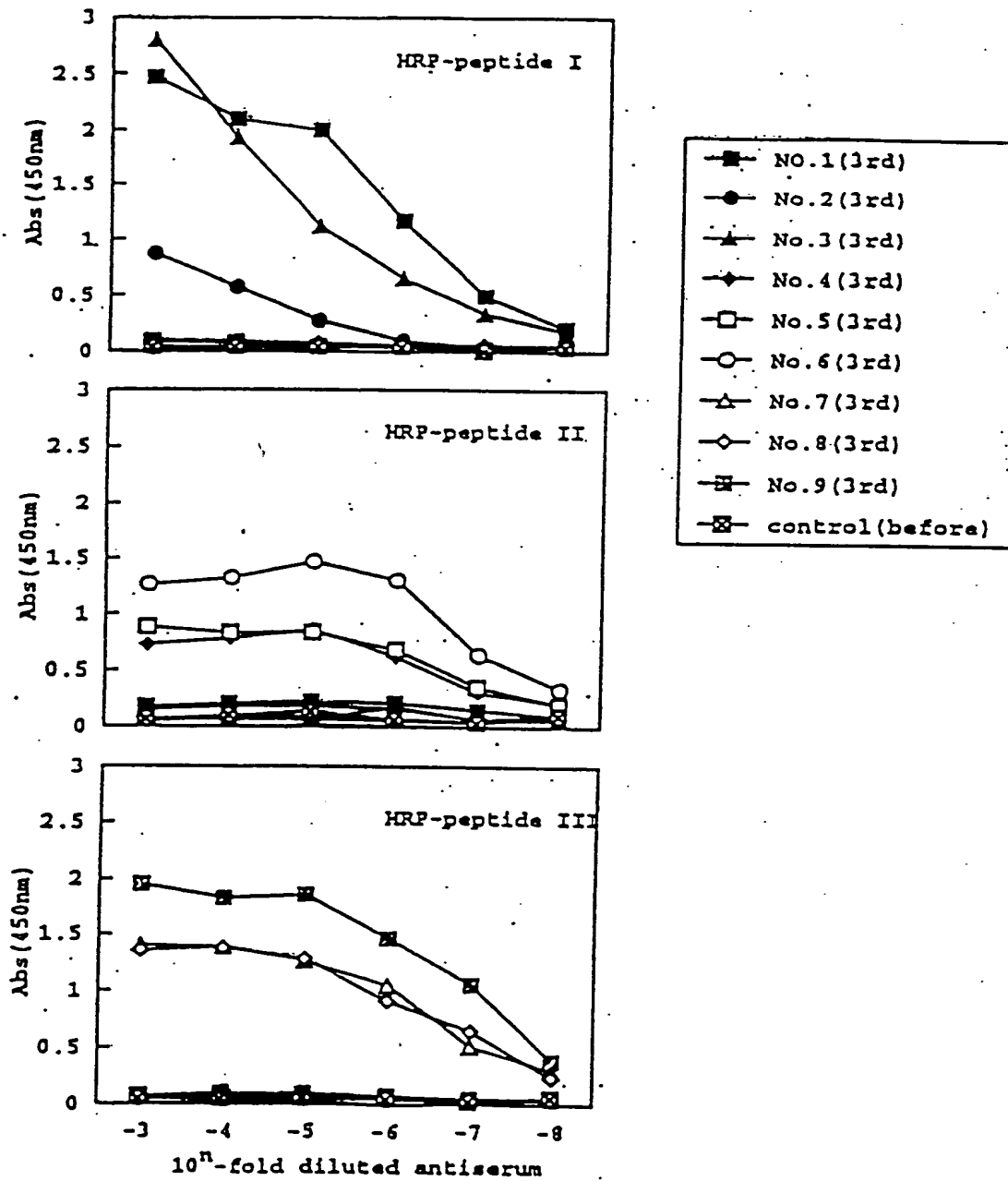


Fig. 51

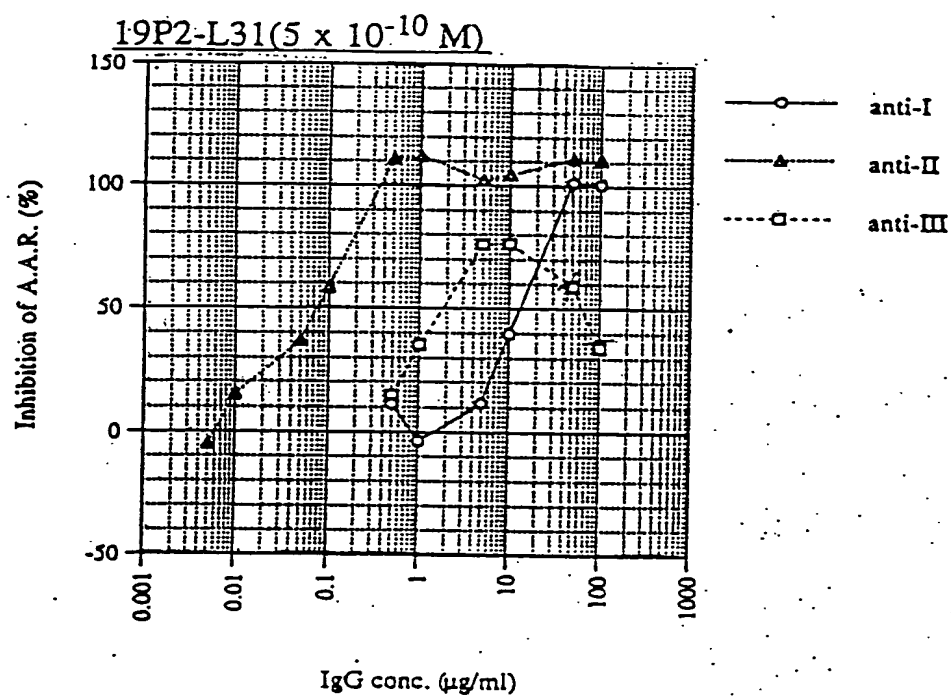


Fig. 52

5' ⁹ ¹⁸ ²⁷ ³⁶ ⁴⁵ ⁵⁴
 ATG ACT TCA GTG GCG GGT GCA AGC AGT GCG CAC GCG GAT TTG TTT TCT GCG GCG
 Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser Gly Pro

⁶³ ⁷² ⁸¹ ⁹⁰ ⁹⁹ ¹⁰⁸
 TCG GCA GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser Glu Ser Asn

¹¹⁷ ¹²⁶ ¹³⁵ ¹⁴⁴ ¹⁵³ ¹⁶²
 GTC TCT GCG AGC GGT GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Val Ser Ala Thr Val Pro Arg Ala Ala Val Thr Pro Phe Gln Ser Leu Gln

¹⁷¹ ¹⁸⁰ ¹⁸⁹ ¹⁹⁸ ²⁰⁷ ²¹⁶
 CCA GTC GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Leu Val His Gln Leu Lys Gly Leu Ile Val Met Leu Tyr Ser Ile Val Val Val

²²⁵ ²³⁴ ²⁴³ ²⁵² ²⁶¹ ²⁷⁰
 GTC GGT GTC GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Val Gly Leu Val Gly Asn Cys Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

²⁷⁹ ²⁸⁸ ²⁹⁷ ³⁰⁶ ³¹⁵ ³²⁴
 CCG GCG AAC GCG AGC AAC TCT GCG AGC GCG AAC GCG GCG GCG GCG GCG GCG
 Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

³³³ ³⁴² ³⁵¹ ³⁶⁰ ³⁶⁹ ³⁷⁸
 AGC TCT GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

³⁸⁷ ³⁹⁶ ⁴⁰⁵ ⁴¹⁴ ⁴²³ ⁴³²
 TCG GTC TCT GGT GCA GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

⁴⁴¹ ⁴⁵⁰ ⁴⁵⁹ ⁴⁶⁸ ⁴⁷⁷ ⁴⁸⁶
 GTC TAC GCA TCT GTC AGC AGC AGC AGC AGC AGC AGC AGC AGC AGC AGC
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Thr Ala Val Asp Arg Tyr Val Val

⁴⁹⁵ ⁵⁰⁴ ⁵¹³ ⁵²² ⁵³¹ ⁵⁴⁰
 CCG GTC GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser Ala Tyr Ala Val

⁵⁴⁹ ⁵⁵⁸ ⁵⁶⁷ ⁵⁷⁶ ⁵⁸⁵ ⁵⁹⁴
 CCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr

⁶⁰³ ⁶¹² ⁶²¹ ⁶³⁰ ⁶³⁹ ⁶⁴⁸
 TCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly

⁶⁵⁷ ⁶⁶⁶ ⁶⁷⁵ ⁶⁸⁴ ⁶⁹³ ⁷⁰²
 TCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr

⁷¹¹ ⁷²⁰ ⁷²⁹ ⁷³⁸ ⁷⁴⁷ ⁷⁵⁶
 TCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu

⁷⁶⁵ ⁷⁷⁴ ⁷⁸³ ⁷⁹² ⁸⁰¹ ⁸¹⁰
 CCG AAC GCG GTC GTC GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg

⁸¹⁹ ⁸²⁸ ⁸³⁷ ⁸⁴⁶ ⁸⁵⁵ ⁸⁶⁴
 CCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala

⁸⁷³ ⁸⁸² ⁸⁹¹ ⁹⁰⁰ ⁹⁰⁹ ⁹¹⁸
 GTC TCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg

⁹²⁷ ⁹³⁶ ⁹⁴⁵ ⁹⁵⁴ ⁹⁶³ ⁹⁷²
 CCG AGC GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His Trp Leu Ala

⁹⁸¹ ⁹⁹⁰ ⁹⁹⁹ ¹⁰⁰⁸ ¹⁰¹⁷ ¹⁰²⁶
 ATG AGC TCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
 Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp Leu His Asp Ser Phe

¹⁰³⁵ ¹⁰⁴⁴ ¹⁰⁵³ ¹⁰⁶² ¹⁰⁷¹ ¹⁰⁸⁰
 CCA GCG GCG CTA GCG AAC ATG GTC TCT TCT GCG GCG GCG AAC AGC GTC GCG GCG
 Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro His

¹⁰⁸⁹ ¹⁰⁹⁸ ¹¹⁰⁷ ¹¹¹⁶
 CCG GCG AAC ATG AGC GTC AGT GTC GTC ATG TCA TCA T'
 Gly Gln Asn Met Thr Val Ser Val Val Ile